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OM protein - protein search, using SW model

Run on: February 14, 2005, 15:03:35 ; Search time 43 Seconds

(without alignments) 1458.915 Million cell updates/sec

Title: US-10-614-076-98
Perfect score: 3406 .

Sequence: 1 MNPNNRSEHTIKVTPNSEL.....SFVSNEKIVYDKEFIPVQL 652

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96226763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 150 summaries

Database : PIR_79.*
1: pi1: *
2: pi2: *
3: pi3: *
4: pi4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3406	100.0	652 2 139811	parasporal crystal
2	94.3	659 2 S10228	parasporal crystal	parasporal crystal
3	2341.5	68.7	A27323	parasporal crystal
4	2152	63.2	JH0261	parasporal crystal
5	1127.5	33.1	S49247	parasporal crystal
6	1124.5	33.0	I40590	cry45 Protein
7	1119	32.9	A48944	parasporal crystal
8	1100.5	32.3	719 2 I39815	insecticidal prote
9	1091.5	32.0	719 2 I39814	insecticidal prote
10	1091.5	32.0	S25383	parasporal crystal
11	1072.5	31.5	S00873	parasporal crystal
12	1060	31.1	I160 2 A40589	parasporal crystal
13	963.5	28.3	1138 2 A48944	parasporal crystal
14	899.5	27.4	655 2 JC7140	protoxin - Bacillus
15	926.5	27.2	1189 2 S0094	parasporal crystal
16	907.5	26.6	823 2 S04181	parasporal crystal
17	906.5	26.6	S02134	parasporal crystal
18	900.5	26.4	A26513	parasporal crystal
19	899.5	26.4	1155 2 JD0002	parasporal crystal
20	899	26.4	1156 2 A29125	parasporal crystal
21	898.5	26.4	1174 2 A42459	parasporal crystal
22	895.5	26.3	1155 2 I39838	parasporal crystal
23	898	26.1	A41052	parasporal crystal
24	886.5	26.0	1176 2 A48970	parasporal crystal
25	876	25.7	1176 2 JT0241	parasporal crystal
26	874	25.7	934 2 A22798	parasporal crystal
27	870	25.5	1176 2 JC2219	parasporal crystal
28	869.5	25.5	1171 2 I40572	parasporal crystal
29	869.5	25.5	1171 2 A37829	parasporal crystal

30	867.5	25.5	A49785	parasporal crystal
31	867	25.5	USBSXH	parasporal crystal
32	866.5	25.4	S32645	parasporal crystal
33	866	25.4	A22617	parasporal crystal
34	866	25.4	S02215	parasporal crystal
35	861.5	25.3	S1145	parasporal crystal
36	845	24.8	S32649	parasporal crystal
37	838.5	24.6	S1146	parasporal crystal
38	828	24.3	S32647	parasporal crystal
39	809	23.8	A29938	parasporal crystal
40	787.5	23.1	B42459	parasporal crystal
41	700	20.6	T18211	hypothetical prote
42	679	19.9	S19106	parasporal crystal
43	665.5	19.5	C32053	parasporal crystal
44	656.5	19.3	USBSBI	parasporal crystal
45	637.5	18.7	I39870	parasporal crystal
46	634.5	18.6	A26558	mosquitocidal prot
47	682	14.2	JC633	delta endotoxin -
48	279.5	8.2	T18211	parasporal crystal
49	245.5	7.2	D32053	parasporal crystal
50	245	7.2	633	parasporal crystal
51	236	6.9	T18213	parasporal crystal
52	233	6.8	A25140	parasporal crystal
53	228.5	6.7	T18212	parasporal crystal
54	228	6.7	S17402	parasporal crystal
55	219.5	6.4	A43647	parasporal crystal
56	215.5	6.3	T18210	delta endotoxin -
57	138	4.1	G90563	lipoprotein [impor
58	129.5	3.8	2139	vitellogenin - yel
59	127.5	3.7	S45768	mitotic spindle pr
60	126	3.7	C97168	glycosyltransferas
61	125.5	3.7	S68218	botulinum neurotox
62	124	3.6	753	maltoesophosphoryl
63	121.5	3.6	1138	membrane nuclease
64	121.5	3.6	2529	toxin-like outer m
65	120.5	3.5	A64635	nontoxic-nonnemagg
66	120	3.5	JC4301	alpha-glucosidase
67	119.5	3.5	F86534	hypothetical prote
68	119.5	3.5	E72305	lactocepin (EC 3.4
69	119	3.5	JC6332	exo-alpha-sialidas
70	119	3.5	AG1710	hypothetical prote
71	118	3.5	A82339	toxin-like outer m
72	118	3.5	T28517	nontoxic-nonnemagg
73	118	3.5	S70582	hypothetical prote
74	117.5	3.4	G70163	maltoesophosphoryl
75	117.5	3.4	T18281	toxin-like outer m
76	117.5	3.4	F82885	hypothetical prote
77	117	3.4	F64489	hypothetical prote
78	117	3.4	S32220	cell wall-associat
79	116.5	3.4	F71479	hypothetical prote
80	116	3.4	A53111	glucose-regulated
81	115.5	3.4	G71605	botulinum neurotox
82	115	3.4	S11455	RAD2 endonuclease
83	115	3.4	A11769	cyclomaltodextrin
84	114.5	3.4	A29517	endoplasmic reticu
85	114.5	3.4	A90206	histidinol-phospho
86	114.5	3.4	G98964	probable permease
87	114.5	3.4	S59823	hypothetical prote
88	114	3.4	E71619	ATP-binding transp
89	114	3.3	A1BSG1	probable pepidogl
90	114	3.3	A3554	hypothetical prote
91	114	3.3	D59105	probable DNA-direc
92	114	3.3	T28426	probable membrane
93	114	3.4	S59823	hypothetical prote
94	113.5	3.3	F90563	ATP-binding transp
95	113.5	3.3	G69820	probable pepidogl
96	113	3.3	A1717	hypothetical prote
97	113	3.3	T21137	hypothetical prote
98	113	3.3	T31536	hypothetical prote
99	113	3.3	AH052	protein tyrosine k
100	112.5	3.3	T18534	probable spinde p
101	112.5	3.3	T50382	ribotryptor protein -
102	112	3.3	T28676	hypothetical prote

103	111	1017	2	T18488	Query Match	100.0%	Score 3406;	DB 2;	Length 652;
104	111	1067	2	T28663	Best Local Similarity	100.0%	Pred. No. 3..1e-20;		
105	111	1658	2	S5101	Mismatches	0;			
106	111	2910	2	T28156	Matches	652;			
107	110.5	520	2	T18124	Conservative				
108	110.5	2485	1	H71621	Qy	1	MNPNNRSEHDTIKTPNSLQTHNQYPLADPNPSTLEBLNQYKFLRMTEDSSTEVLDS	60	
109	110	725	2	T19994	Db	1	MNPNNRSEHDTIKTPNSLQTHNQYPLADPNPSTLEBLNQYKFLRMTEDSSTEVLDS	60	
110	110	814	1	C40618					
111	110	1616	2	T16600	61	TIVDAVGTQISIVGQIIGVGDPAQALTSEYQSFNLNTWPSDADPKAFAQAEVLFIDK	120		
112	109.5	957	2	H97800	61	TIVDAVGTQISIVGQIIGVGDPAQALTSEYQSFNLNTWPSDADPKAFAQAEVLFIDK	120		
113	109.5	986	2	S30596					
114	109.5	1103	2	H81884	121	KIEEYAKSKALAEQLQNLNFEDVNAANSWKTKPLSLRSKRSODRIRLEFSQAESHEPN	180		
115	109.5	1119	2	B70126	Qy				
116	109	726	2	S62180	Db	121	KIEEYAKSKALAEQLQNLNFEDVNAANSWKTKPLSLRSKRSODRIRLEFSQAESHEPN	180	
117	109	804	2	S01358					
118	109	1202	1	S03362	181	SMPSFAVSKPEVLFPTQAQANTHLLKLKDAAQVEGEEWGYSSDVAEPYHQKLQTORY	240		
119	109	2819	2	A50551	Qy				
120	108.5	640	2	T0754	Db	181	SMPSFAVSKPEVLFPTQAQANTHLLKLKDAAQVEGEEWGYSSDVAEPYHQKLQTQY	240	
121	108.5	775	1	VPKRW6					
122	108.5	4450	2	U70340	241	TDHCYNWYWNGLNGLRGSTYDAWKFKFRFREMTLTVDLFLPVFPYDRLYSKGVKTEL	300		
123	108.5	4550	2	T18440	Qy				
124	108	593	2	F64523	Db	241	TDHCYNWYWNGLNGLRGSTYDAWKFKFRFREMTLTVDLFLPVFPYDRLYSKGVKTEL	300	
125	108	851	2	S50670					
126	108	986	2	H91565	Qy	301	TRDIFTPIFSINTLQEYQPTELSIENSTRKPHFLDYLQGIEFHTRLQPGYFGKDSFNYW	360	
127	107.5	1086	2	T43266	Db	301	TRDIFTPIFSINTLQEYQPTELSIENSTRKPHFLDYLQGIEFHTRLQPGYFGKDSFNYW	360	
128	107.5	1086	2	T40242					
129	107.5	1468	1	S30818	Db	301	TRDIFTPIFSINTLQEYQPTELSIENSTRKPHFLDYLQGIEFHTRLQPGYFGKDSFNYW	360	
130	107.5	1790	1	S27772					
131	107	300	2	T08453	Qy	361	SGNYTVERPPIGSKTTSPPYGDKSSTEPVQKLSSITSPPYGDKSSTEPVQKLSSITSPPYGDKS	420	
132	107	1048	2	H64459	Db	361	SGNYTVERPPIGSKTTSPPYGDKSSTEPVQKLSSITSPPYGDKSSTEPVQKLSSITSPPYGDKS	420	
133	107	1599	2	S22737					
134	107	2178	2	S55805	421	VTKYDVSQYDQKNETISTOTYDKSRKNNGHVAQDSIDQLPETTDEPLEKAYSHOLNYAE	480		
135	107	2364	2	I40884	Qy				
136	107	3262	2	AH2137	Db	421	VTKYDVSQYDQKNETISTOTYDKSRKNNGHVAQDSIDQLPETTDEPLEKAYSHOLNYAE	480	
137	107	4196	2	T41274					
138	106.5	822	2	AB5207	Qy	481	CFLMQRDRGRTIPPFWTHRSVDFENTIDAEKITOLPVVKAIALSGGASIEGPGBTGGNL	540	
139	106.5	834	2	BB2340	Db	481	CFLMQRDRGRTIPPFWTHRSVDFENTIDAEKITOLPVVKAIALSGGASIEGPGBTGGNL	540	
140	106.5	891	2	B89357					
141	106.5	945	2	A62714	Db	481	CFLMQRDRGRTIPPFWTHRSVDFENTIDAEKITOLPVVKAIALSGGASIEGPGBTGGNL	540	
142	106.5	1272	2	S60999					
143	106.5	1279	2	B64109	Qy	541	LFLKESSNIAKFKYTLNSALLQYVRVRYASTNLFLVQNSNDLFLVYIXNTMK	600	
144	106.5	1959	2	AG1085	Db	541	LFLKESSNIAKFKYTLNSALLQYVRVRYASTNLFLVQNSNDLFLVYIXNTMK	600	
145	106.5	4563	1	LPRUB					
146	106	485	2	E70363	Qy	601	DDDLTYQTFLATINNSMGSGDKNELLIGAESFYNEKIYIDKIEFIPYQOL	652	
147	106	659	1	A62228	Db	601	DDDLTYQTFLATINNSMGSGDKNELLIGAESFYNEKIYIDKIEFIPYQOL	652	
148	106	3.1	2	A49777					
149	106	1291	2	S46331	Qy				
150	106	2077	2	T44178	Db				

ALIGNMENTS

RESULT 2

S10228

parasporal crystal protein cry3Bal - *Bacillus thuringiensis* (fragment)
N;Alternate names: Coleopteran-active parasporal crystal protein; delta-a-endotoxinC;Species: *Bacillus thuringiensis*

C;Accession: S10228

R;Sick, A.; Gaertner, P.; Wong, A.

A;Nucleic Acids Res. 18, 1305, 1990

A;Title: Sequence of a coleopteran-active toxin gene from a new isolate of *Bacillus thuringiensis* (fragment)

A;Reference number: S10228; PMID:2320431

A;Accession: S10228

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-59 <TC>

A;Gene: cryIIIB

A;Cross-references: UNIPROT:P17969; EMBL:XL7123; NID:940258; PID:CAA34983.1; PMID:940259

C;Keywords: parasporal crystal protein

C;Superfamily: delta-endotoxin; toxin

C;Genetics:

C;Supertaxonomy: cryIIIB

C;Keywords: parasporal crystal protein

RESULT 1

I39811

Parasporal crystal protein cry3Bb1 - *Bacillus thuringiensis*C;Species: *Bacillus thuringiensis*

C;Accession: I39811

C;Title: Characterization of two genes encoding *Bacillus thuringiensis* insecticidal crys

A;Reference number: I39811; MUID:9319147; PMID:1476436

A;Accession: I39811

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-652 <RES>

A;Cross-references: UNIPROT:Q06117; GB:M89794; PID:9142729; PID:AAA22334.1; PMID:9142730

A;Gene: cryIIIB

A;Cross-references: UNIPROT:P17969; EMBL:XL7123; NID:940258; PID:CAA34983.1; PMID:940259

C;Keywords: parasporal crystal protein

C;Superfamily: cryIIIB

C;Keywords: delta-endotoxin; toxin

C;Genetics:

C;Supertaxonomy: cryIIIB

C;Keywords: parasporal crystal protein

Qy	1	MNPNNRSEHDITKTPNSLQTNHNPYPLADNPNSTLLEFLNLYKEFLRMTEDSSTEVLDS	60	A;Title: Characterization of the coleopteran-specific protein gene of <i>Bacillus thuringiensis</i>
Db	9	MNPNNRSEHDITKTPNSLQTNHNPYPLADNPNSTLLEFLNLYKEFLRMTADNSTEVLOSS	68	A;Reference number: A29987 A;Accession: A29987 A;Molecule type: DNA A;Residues: 9-652 <MCP>
Qy	61	TVKDAVGTGIVSIVGQILGVGVPPFAGALTFSYOSFLNTIWPSPDAPWKFMAQVBVLIDK	120	A;Experimental source: var. <i>tenebrionis</i> R;Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.
Db	69	TVKDAVGTGIVSIVGQILGVGVPPFAGALTFSYQSFLNAIWPSPDAPWKFMAQVBVLIDK	128	Proc. Natl. Acad. Sci. U.S.A. 84: 7056-7060, 1987
Qy	121	KIEEYAKSKALAEGLQNLNFEDTYNALSWKCTPLSLRSKSDRIRLFQSQESHRN	180	A;Title: Molecular cloning and characterization of the insecticidal crystal protein gene
Db	129	KIEEYAKSKALAEGLQNLNFEDTYNALSWKCTPLSLRSKSDRIRLFQSQESHRN	188	A;Reference number: A28407 A;Accession: A28407 A;Molecule type: DNA A;Residues: 9-652 <SEK>
Qy	181	SMPSPAVSKPEVLPIPTYAOANTHLLIKDKDAQVGEETGYSSSDVAEYHROLKLTKQY	240	A;Experimental source: var. <i>Tenebrionis</i> R;Adams, L.P.; Mattheyses, S.; O'Hara, P.; Petersen, A.; Guertler, H.
Db	189	SMPSPAVSKPEVLPIPTYQAANTHLLIKDKDAQVGEETGYSSSEDIAEYQQRQLKLTQY	248	Mol. Microbiol. 14: 381-389, 1994
Qy	241	TDHCVNWNWAVGLNGLRGSTYDAWKFNRFRRMELTTLVLIVLFPFYDYLRYSKGVKTEL	300	A;Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized strain NB176, a mutant of strain NB176, a mutant of strain NB176
Db	249	TDHCVNWNWAVGLNGLRGSTYDAWKFNRFRRMELTTLVLIVLFPFYDYLRYSKGVKTEL	308	A;Reference number: S60781; PMID: 7830581 A;Accession: S60781 A;Status: nucleic acid sequence not shown; translation not shown
Qy	301	TRDIFTDPFSLNTLQEYKPTFELTSNRSRKPHLFDYLGQIEFHTRLQFGYFSKDSFNYW	360	A;Molecule type: DNA A;Residues: 9-652 <ADA> A;Cross-references: ENBL:U10985; NID:9506182; PID: AAC43266.1; PID:9514312
Db	309	TRDIFTDPFSLNTLQEYKPTFELTSNRSRKPHLFDYLGQIEFHTRLQFGYFSKDSFNYW	368	A;Experimental source: var. <i>Tenebrionis</i> strain NB176, a mutant of strain NB176
Qy	361	SGNYVETRISIGSSKTTISPPYGDKSTEVQKSLFDGKVYRJANTDAAWPNKGKVYLG	420	A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994 R;Nu, S.J.; Dean, D.H.
Db	369	SGNYVETRISIGSSKTTISPPYGDKSTEVQKSLFDGKVYRJANTDAAWPNKGKVYLG	428	J. Mol. Biol. 255: 628-640, 1996
Qy	421	VTKVDFSQYDQNETSTOTYDSKRNGHVSAAQPSDIDQLPETTDEPLEKAYSHOLNAYA	480	A;Title: Functional significance of loops in the receptor binding domain of <i>Bacillus thuringiensis</i>
Db	429	VTKVDFSQYDQNETSTOTYDSKRNGHVSAAQPSDIDQLPETTDEPLEKAYSHOLNAYA	488	A;Reference number: S63137; PMID: 96163559; PMID: 8568902 A;Contents: annotation R;Donovan, W.P.; Gonzalez, J.M.
Qy	481	CFLMDQRRTIPFPTWTHSVDFNTTIDELEKITOLPVVKAYASSGASIEGGCFGTGQNL	540	Mol. Gen. 214: 365-372, 1988
Db	489	CFLMDQRRTIPFPTWTHSVDFNTTIDELEKITOLPVVKAYASSGASIEGGCFGTGQNL	548	A;Title: Isolation and characterization of EG2158, a new strain of <i>Bacillus thuringiensis</i>
Qy	541	LFLKESSNSIAKFTVTLNSAALLORYRFLYRIRASTNLFLVONSNNDELVLTINKTMK	600	A;Reference number: I39812; PMID: 89112339; PMID: 3146015 A;Accession: I39812 A;Status: preliminary; translated from GB/EMBL/DDJB
Db	549	LFLKESSNSIAKFTVTLNSAALLORYRFLYRIRASTNLFLVONSNNDELVLTINKTMK	608	A;Molecule type: DNA A;Residues: 9-652 <RES> A;Cross-references: GB: M37207; NID: g142735; PID: g142736
Qy	601	DDDLITYQTDFLATNSNMGSQGDNELITGAESFSVSNEKIVYDKEIFIPVQ	651	A;Experimental source: strain EG2158 R;Reixeira De Souza, M.; Leclade, M.M.; Lereclus, D.
Db	609	DDDLITYQTDFATNSNMGSQGDNELITGAESFSVSNEKIVYDKEIFIPVQ	659	J. Bacteriol. 175: 2932-2940, 1993
Qy	610	DDDLITYQTDFATNSNMGSQGDNELITGAESFSVSNEKIVYDKEIFIPVQ	651	A;Title: Full expression of the cryIIIA toxin gene of <i>Bacillus thuringiensis</i> requires a delta-endotoxin gene A;Reference number: I39813; PMID: 93259939; PMID: 8491716 A;Accession: I39813 A;Status: preliminary; translated from GB/EMBL/DDJB
Db	618	DDDLITYQTDFATNSNMGSQGDNELITGAESFSVSNEKIVYDKEIFIPVQ	659	A;Molecule type: DNA A;Residues: 9-58 <RE2> A;Cross-references: GB: L03393; NID: 9304150; PMID: AAA50255.1; PID: g551698 A;Gene: cryIIIA C;Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin
Qy	623	RESULT 3		Query Match Score 68.7%; Best Local Similarity 68.6%; Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;
A2	323	parasporal crystal protein cry3Aa1 - <i>Bacillus thuringiensis</i>		Y Q 1 MNPNRNRSEHDITKTPNSLQTNHNPYPLADNPNSTLLEFLNLYKEFLRMTEDSSTEVLDS 60
N;Alternate names: Coleopteran-specific insect control protein; crystal protein cryc; species: <i>Bacillus thuringiensis</i>		C;Accession: A27323; A26853; A28407; S60781; I39813		Db 9 MNPNRNRSEHDITKTPNSLQTNHNPYPLADNPNSTLLEFLNLYKEFLRMTADNTEALDS 68
C;Accession: 19-Nov-1988 #sequence revision 19-Nov-1988 #text change 09-Jul-2004		R;Herrnstadt, C.; Gilroy, T.B.; Sobieski, D.A.; Bennett, B.D.; Gaertner, F.H.		Qy 61 TVKDAVGTGIVSIVGQILGVGVGFAGALTFSYOSFLNTIWPSPDAPWKFMAQVEVLIDK 120
R;Hoefte, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.		Gene 57: 37-46, 1987		Db 69 TRKDVIQKIGISVGDLGVGFQGALVSFTNLENLTIWPSE-DPKAFMEQVALMDQ 127
A;Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active delta-endotoxin gene		A;Reference number: A27323; PMID: 282880		Qy 121 KIEBIAKSKALAEGLQGLNNFEDYVNALNSWKTPLSLRSKSDQRIRFLSQAESHRN 180
A;Accession: A27323		A;Molecule type: DNA A;Residues: 1-652 <HER>		Db 128 KIADYAKNKALAEGLQGLNNFEDYVNALNSWKTPLSLRSKSDQRIRFLSQAESHRN 187
A;Cross-references: UNP:PROT:Q9S6N9; GB:M22472; NID:9142733; PID:9142734		A;Experimental source: strain San Diego		A;Cross-references: GB:Y00420; PID:940252; PID:CAA8482.1; PID: g10253
R;Seurinck, J.; Van Houtven, A.; Vaeck, M.		R;Hoefte, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.		R;McPherson, S.A.; Perak, F.J.; Fuchs, R.U.; Marrone, P.G.; Lavrik, P.B.; Fischhoff, D.
A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of <i>Bacillus thuringiensis</i>		A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of <i>Bacillus thuringiensis</i>		Bio/Technology 6, 61-66, 1988
A;Reference number: A26853; PMID: 88015559; PMID: 365880		A;Accession: A26853		181 SMPSEAVSKPEVFLPLPTYAOANTHLLIKDAQVGEWSSEDVAEFYHROLKLTQY 240
A;Molecule type: DNA A;Residues: 9-652 <HOE>		A;Experimental source: var. <i>tenebrionis</i>		182 SMPSEAVSKPEVFLPLPTYAOANTHLLIKDAQVGEWSSEDVAEFYHROLKLTQY 247

Y	241	TDHCVANVNGLNGLRGSTYDAWKFRMRMELITVLDLIVLFPPFYDIRLYSKGVKTEL	300
b	248	TDHCVKRVNVGLDKLRGSSYESWNVNFYRMRMELITVLDLIALFPLDVRLPKEVETL	307
Y	301	TRDIFTDPIFSINTLQEQPTFLSIEENIRKPHLFDFLYQGIEFHTRLOGYIKGDSENW	360
b	308	TRDVLIDPVGAVNLRGYGTFSMNEYIRKPHLFDFYLHRIQPTRFQPGYCNDSFNW	367
Y	361	SGNYVETRPSIGSSKTISPFYGBKSTEPVQLSFDGKQYRTIANTDVAAPNGKVYLG	420
b	368	SGNYVSTRPSIGSNDIITSPFYGKRSSEPVQNLIFENGKRYAVANTILAWPSA-VYSG	426
Y	421	VTRUDFESQYDDQNETSTOTYDQRNNGHVSACQSDIDOLPPETDEPLEKAYSHQLNNTA	480
b	427	VTKVEFSQYDQTEASOTYDQRNNGAVS-WNSIDQLPPETDEPLEKGYSQHQNNTW	485
Y	481	CFLMDRGTIPFTWHTSRVDENTIDAKBKTOLPNUKAYALSASGASLIEGPFTGCRN	540
b	486	CFLMGSRCITPVLTWTHKSVDFTFMIDSKKTOLPNUKAYLQSGASTVAGPFTGGDI	545
Y	541	LFLKESNSIAKPVTLNSAALLORYRPYRASYTNLRLFVQNSNNDFLVIVNKTMK	600
b	546	IQCET-NGSFRATIVT-PDVSYSKQXARYTHASQTFELTSLDGAPPNOYDPKTINK	603
Y	601	DDDLITYCQTDLATNSNMGFSDGKNEELITGAESFVSKYIYDKEBIFPV	650
b	604	GDTLTYNSFLASSSTPFELSG--NNLQIGVTGSLAGDKVYIDKEBIFPV	651

RESULT 4

JH0261 Bacillus thuringiensis subsp. kurstaki (strain BTI)
 parasporal crystal protein cry3Cal - Bacillus thuringiensis subsp. kurstaki (strain BTI)
 parasporal crystal protein cryIIID
 Alternative names: parasporal crystal protein cryIIID
 C.Species: Bacillus thuringiensis subsp. kurstaki
 C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 @text_change 09-Jul-2004
 C;Accession: JH0261; S11944
 R;Lambert, B.; Theunissen, W.; Aguda, R.; Van Audenhove, K.; Decock, C.; Jansens, S.; Seurinckx, A.;Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crystal protein
 A;Reference number: JH0261; PMID:92184108; MUID:1544571
 A;Accession: JH0261
 A;Molecule type: DNA
 A;CrossReferences: 1-649 <LM>
 A;CrossReferences: UNIPROT:Q45744; EMBL:X59797; PIDN:CAA42469_1; PID:g40287; PID:g4028

Qy	301 TRDIFDPFISLNTLQEYGPFLSLENSTEKPKHFLDYLQGIEFHTRLQEPYFGKDSFNTW	360
Db	298 TRDVLDPPIAVNNNNGGYGTFSNTINYTRKPHFLYLHQFHSLLQPGTGSNTW	357
Qy	361 SGNVETRPSIGSSKTTTSPPYGDKSTEPIQKLSPGQKYRTIANTDVAAPNG---	K 416
Db	358 SGNYVSTRSSIGSDTEIRSPFGNKSTLDVQNLEFGKEVKYFRAVANGNLAWPVGJGGTK	417
Qy	417 VYLGTVKVDPSOYDOKNETSTQTYPSKRNGHVSQDSIDQLQPPTTDEPLEKAWSHOL	476
Db	418 IHSGVTKVQFSQINRDRDEVRTOYTYSKRNVGGI - VPDSIDOLQPPTTDESIEKAWSHOL	476
Qy	477 NYAECFLMDQRGTTIPFTWTRSVDFENTIDAEKTOOLPVKAYALSSQSGEGRGFT	536
Db	477 NYVRCFLQGGERIPVFTWTRSVDFNTLOSEKTOIPFKAFILVNNTSVVAGPGFT	536
Qy	537 GGNLFLKESNSIAKEFKVTLNSAALLQRYVRIRYASTTNLRLFVQNSNNDFLVYINK	596
Db	537 GDIIKCTNGS-GLTLYTPAPLTVSKTYKIRIATSTSQRFGDLGSYTHS1SVEFDK	595
Qy	597 TNKKDDITYQTPLATTNSNNGFGSKDNELLGAEFSVNEK1YDKIEFIPV	650
Db	596 TMDKGNTLYTNSFLNSVSRPIEISGG-NKIVGVSQGTSGDEVYDKEFIPM	648
RESULT 5		
S49247	parasporal crystal protein cry9cgal [validated] - <i>Bacillus thuringiensis</i>	
N;Alternate names:	parasporal crystal protein cryIH	
C;Species:	<i>Bacillus thuringiensis</i>	
C;Date:	01-Dec-2000 #text_change 09-Jul-2004	
C;Accession:	A59350; S99247	
R;Lamberton, B.; Buyse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinckx, A.; Appl. Environ. Microbiol. 62, 80-86, 1996		
A;Title:	A <i>Bacillus thuringiensis</i> insecticidal crystal protein with a high activity against corn borer and other	
A;Reference number:	A59350; MUID:9614404; PMID:8577215	
A;Accession:	A59350	
A;Molecule type:	DNA	
A;Residues:	1-115 <LAM>	
A;Cross-references:	UNIPROT:Q45733; EMBL:227527; NID:9547554; PIDN:CAA85764.1;	
A;Experimental source:	serovar tolworth	
C;Comment:	This parasporal crystal protein, active against corn borer and other	
C;Superfamily:	parasporal crystal protein	
C;Keywords:	delta-endotoxin	
Query Match	Score 1127.5; DB 1; Length 1157;	
Best Local Similarity	36.1%; Pred. No. 4.8e-64;	
Matches 250;	Ni smatches 217; Indels 77; Gaps 19;	
Qy	1 MNPNRSEHDITKVTSPNSELQTNHN-QYPLADNPNSTLELNKREFLRLMTEDSSTEVLDN	59
Db	1 MNTRNQNEYELID-APHCGCPSDDDVRYPLASDPAALQMNMYKYLQMTDEDYDSYIN	59
Qy	60 STV--KDAGTG-SVYQGQILGVYGVPFAGALTSPYQOSPLNTIWP-SDADPWKFMAQV	114
Db	60 PSLSISGRDQATLTYVGLTGAQVPSQIVSPYQFLNLTPVNDTAIWEFMRQV	119
Qy	115 EVLDKKIEEYAKSKALABLOGLQNONFEDYVNAWSKKTPSLIS-KRSQDRITRELFSQ	173
Db	120 EBLVNOQITEFARNQNLARLQGLGDSFNVYQRSQLNW---LADNDTRNLSSVRAQFIA	175
Qy	174 AESHRNMSMPFAVSKPEVLFPTYQAAHTHLILKDAQVFGENGYSSSEDVAEYHRO	233
Db	176 LDLDIFVNAIPAVNGQOVPLLSVQAQVNLHLLILKDAISLTFGWTQEISTYDQR	235
Qy	234 LKLTQQTDHCYNWXNGVGLNGLRGSTDANWYKFNFRREMLTVLDDLVLEPPFYDRLYS	293
Db	236 LEFTAKTNYCETWYNTGLDRGNTBWSRYHQFRREMLVVLDDVALFPYYDYLRYLP	295
Qy	294 KGVKTELTRDIFDPIF----SLNTLQEYGP---TFLSIENS-IRKPHLFDYLOGIEF	343
Db	296 TGSNPOLTREVTDPIVFNPANPVGCRWGTNPNTFSELAHFIRPFLDRNLSTI	355

Qy	344 HTRLQPGYFGKDSFENYWSGNVETRPSIGSSKTTITSPFY-----GDKSTEPVQ 391	Qy	344 HTRLQPGYFGKDSFENYWSGNVETRPSIGSSKTTITSPFYGDKST-----EPVQKULSPDGQKRY 401
Db	356 SSNRP-----YSSNFDYWSNL-----RRSYLNDSAQEDSYGLITTRATTNPVGUDGTNRIE 411	Db	345 YELIS-----RSNTQYMMNGCHRLSFRPIGALANTSTQ----GSTNTSINPV-TLQTSRVDY 399
Qy	392 KLSFDGOKYRTIANTDVAAPNGKRYLGVYKVDQYDQNETSTOTYDSKRNNNGHVS 451	Qy	402 RTIANTDVAAPNGKRYLGVYKVDQYDQNETSTOTYDSKRNNNGHVS----QDSID 457
Db	412 STAVDFSLALIGYGVNRASFVPGQLFLNGTT-----SPANGGERD 451	Db	400 RTSLAGLNLFTOPVN-GVPRDF---HWKEKPTLPASDNYYLGAGVGTQLDQSEN 454
Qy	452 AODSIDQLPETTDEPLEKAYSHOLNYAECFLMQRDR-----GTIPFETWTHRSVDF 504	Qy	458 QLPETTDEPLEKAYSHOLNYAECFLMQRDRGTFPFTWTHRSVDFNTIDARKITQLPV 517
Db	452 LYDNTDELPPDES---TSSTHASHVFFSFQINQA-SIANAGSVTPVWTRRDVLN 507	Db	455 ELPETTGPNYESYSHRLSHIGLISASHVKALV--YSWTHRSADRNTTIEPNSTQIPL 512
Qy	505 NTDAEKITOLPVKAYALASSGASLTIEGGCPTGGNLFLKESSNSIAKEFKTLNSAALLQ 564	Qy	518 VKAYALSSGASLIEGGCPTGGNLFLKESSNSIAKEFKTLNSAALLQYVRYASTN 577
Db	508 NTIPNPRITOLPLVPLKASAVPSGRTVLYKGQGFTGGIL-RRTTNGCTGTRVTVNS-PITQ 565	Db	513 VRAFNLSGGAAVVRGPGETGGDLU-RRNTGPGDGRIRMIN-BPEAQPYVRVRYASTD 570
Qy	565 RYRVRVYASTTNRLPVONSNNPLVIVINKTMKDDDTYQTF---DIAFT---NSNM 618	Qy	578 LRFLVQ-----NSNNDPLVIVINKTMKDDDTYQTFDLATNSNMGSQGDKNELITGA 631
Db	566 QYRLRVRFASTGNFSIRVLRGGSIGDVRGSTMNRGQELTYESSFTREFTTGPFNPPF 625	Db	571 LQHTHSINGKAQNQN-----FSATMNMRGEDLDYKTFRTIGFTTPFSFSDVOSTFTIGA 624
Qy	619 GFSGDKNELIJGAEFSVNEKIYDKEFIPV 650	Qy	632 ESFVSEKLYIDKIEFIPVOL 652
Db	626 TFTQAQEILTVNAEGVSTGEYIYDRIEIPV 657	Db	625 WNFSSGNVEVYDRIEFVPEV 645
RESULT 6			
140590	CRY465 protein - Bacillus thuringiensis	Qy	A48944
C;Species: Bacillus thuringiensis			parasporal crystal protein cryAa1 - Bacillus thuringiensis
C;Accession: 140590			N;Alternate names: parasporal crystal protein cryAa1
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			C;Species: Bacillus thuringiensis
Appl. Environ. Microbiol. 61, 2422-2401, 1995			C;Date: 19-Dec-1993 #Sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			R;Lambert, B.; Hofte, H.; AnnyB, K.; Jangens, S.; Soetaert, P.; Peferoen, M.
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			Appl. Environ. Microbiol. 58, 2536-2542, 1992
A;Status: preliminary; translated from GB/EMBL/DBJ			A;Title: Novel <i>Bacillus thuringiensis</i> insecticidal crystal protein with a silent activit
A;Molecule type: DNA			A;Reference number: A48944; MUID: 92384571; PMID: 1514800
A;Residues: 1-719 <RES>			A;Contents: BTS137J
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 7			
140590	CRY465 protein - Bacillus thuringiensis	Qy	A48944
C;Species: Bacillus thuringiensis			parasporal crystal protein cryAa1 - Bacillus thuringiensis
C;Accession: 140590			N;Alternate names: parasporal crystal protein cryAa1
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			C;Species: Bacillus thuringiensis
Appl. Environ. Microbiol. 61, 2422-2401, 1995			C;Date: 19-Dec-1993 #Sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			R;Lambert, B.; Hofte, H.; AnnyB, K.; Jangens, S.; Soetaert, P.; Peferoen, M.
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			Appl. Environ. Microbiol. 58, 2536-2542, 1992
A;Status: preliminary; translated from GB/EMBL/DBJ			A;Title: Novel <i>Bacillus thuringiensis</i> insecticidal crystal protein with a silent activit
A;Molecule type: DNA			A;Reference number: A48944; MUID: 92384571; PMID: 1514800
A;Residues: 1-719 <RES>			A;Contents: BTS137J
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 8			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;
Appl. Environ. Microbiol. 61, 2422-2401, 1995			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
A;Status: preliminary; translated from GB/EMBL/DBJ			C;Superfamily: parasporal crystal protein
A;Molecule type: DNA			C;Keywords: delta-endotoxin
A;Residues: 1-719 <RES>			A;Accession: A48944
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 9			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;
Appl. Environ. Microbiol. 61, 2422-2401, 1995			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
A;Status: preliminary; translated from GB/EMBL/DBJ			C;Superfamily: parasporal crystal protein
A;Molecule type: DNA			C;Keywords: delta-endotoxin
A;Residues: 1-719 <RES>			A;Accession: A48944
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 10			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;
Appl. Environ. Microbiol. 61, 2422-2401, 1995			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
A;Status: preliminary; translated from GB/EMBL/DBJ			C;Superfamily: parasporal crystal protein
A;Molecule type: DNA			C;Keywords: delta-endotoxin
A;Residues: 1-719 <RES>			A;Accession: A48944
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 11			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;
Appl. Environ. Microbiol. 61, 2422-2401, 1995			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
A;Status: preliminary; translated from GB/EMBL/DBJ			C;Superfamily: parasporal crystal protein
A;Molecule type: DNA			C;Keywords: delta-endotoxin
A;Residues: 1-719 <RES>			A;Accession: A48944
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 12			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;
Appl. Environ. Microbiol. 61, 2422-2401, 1995			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
A;Status: preliminary; translated from GB/EMBL/DBJ			C;Superfamily: parasporal crystal protein
A;Molecule type: DNA			C;Keywords: delta-endotoxin
A;Residues: 1-719 <RES>			A;Accession: A48944
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 13			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;
Appl. Environ. Microbiol. 61, 2422-2401, 1995			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
A;Status: preliminary; translated from GB/EMBL/DBJ			C;Superfamily: parasporal crystal protein
A;Molecule type: DNA			C;Keywords: delta-endotoxin
A;Residues: 1-719 <RES>			A;Accession: A48944
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 14			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;
Appl. Environ. Microbiol. 61, 2422-2401, 1995			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
A;Status: preliminary; translated from GB/EMBL/DBJ			C;Superfamily: parasporal crystal protein
A;Molecule type: DNA			C;Keywords: delta-endotoxin
A;Residues: 1-719 <RES>			A;Accession: A48944
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 15			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			Matches 252; Conservative 135; Mismatches 229; Indels 65; Gaps 18;
Appl. Environ. Microbiol. 61, 2422-2401, 1995			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> tonocidus.			Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
A;Reference number: 133814; MUID: 95314293; PMID: 7793960			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
A;Status: preliminary; translated from GB/EMBL/DBJ			C;Superfamily: parasporal crystal protein
A;Molecule type: DNA			C;Keywords: delta-endotoxin
A;Residues: 1-719 <RES>			A;Accession: A48944
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; PIDN:9467234; PID:94672			A;Status: preliminary
C;Genetics:			A;Molecule type: DNA; protein
C;Gene: cry465			A;Residues: 1-1138 <LAM>
C;Superfamily: parasporal crystal protein			A;Cross-references: UNIPROT:Q03749; GB:M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761
RESULT 16			
140590	CRY465 protein - Bacillus thuringiensis	Qy	1 MNPNNRSEHDTI-----KVTPNSELQTINHQYPLADNPNSTLEELNKEFIRMEDDS 53
C;Species: Bacillus thuringiensis			Query Match Score 1124.5; DB 2; Length 719;
C;Accession: 140590			Best Local Similarity 37.0%; Pred. No. 3.7e-64;
R;Sh			

Qy 349 PGYFGKDSFNTWGSNVETEPDSIGSKITISPEYGDKSSTEPVQK--LSFDGOKVYRTIAN 406
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 Db 348 PDLF----YWAHKVSFKKS-EQSNLYTGTG-Y-KTGGYISSLGAYSPHGNIDYRTLAA 399
 Qy 407 TDVAAPWNGKYLGVTTKVDPSQYDQNESTQTYDSKRNGHVAQSDIDQLPPTDE 466
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 Db 400 PSVVFITYQN-GTQEVEFTGKV&HYDGNKDY 448
 Qy 467 PLEKAYSHOLNAYAECFLMOD---RREGTIPFTWTHRSDFENTIDAEEKITQLPVYKAYA 523
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 Db 449 PTHEKTHRLCATAFKSTPDKNATIPPSWTHRSAEYNYRYPNKTICKPAVKYTKL 508
 Qy 524 SSSASLIEPGPTGGNLFLKESSNSIAKPKVYTNSAALLQRYVRIRYRZASTINLRLFVQ 583
 Qy :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 Db 509 DDPSTVVKGPGPFTGGDILV-KRGSTGTVGDIAKATVNS-PLSOKYKVRVRA 557
 Qy 584 NSNNDFLVYIN-----KTMNKDDDTYQTFPLATINNSMGFSGDKNELITG 630
 Qy :|||: :|||: :|||: :|||: :|||:
 Db 558 NVSGQFY-NINDKINTLQFKONTVNTIGEGLTYGSFGVIEYSTTIOQPDPDEHPKITH 616
 Qy 631 AEEFVSNEKIXYDKEIFTPVQL 652
 Qy :|||: :|||:
 Db 617 LSDLSNNSSSPYVDSIEFIPVVD 638

RESULT 8

I39815 Insecticidal protein cryv - Bacillus thuringiensis
 C;Species: Bacillus thuringiensis
 C;Accession: I39815 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

R;Gleave, A.P.; Williams, R.; Hedges, R.J.
 Appl. Environ. Microbiol. 59, 1663-1687, 1993
 A;Title: Screening by Polymerase chain reaction of *Bacillus thuringiensis* serotypes for
iensis subsp. *kurstaki*.
 A;Reference number: I39815; MUID:8517758
 A;Accession: I39815
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-719 <RES>
 A;Cross-references: GB:L36338; NID:g540281; PID: AAC36999.1; PMID: 7739360
 C;Genetics:

A;Gene: cryV
 C;Superfamily: parasporal crystal protein
 C;Parasporal crystal protein

Query Match Score 1100.5; DB 2; Length 719;

Best Local Similarity 36.6%; Pred. No. 1.3e-62; Mismatches 231; Indels 63; Gaps 19; Matches 249; Conservative 137; Mismatches 232; Indels 63; Gaps 19;

Qy 1 MNPNNSEHDITI-----KVTPNSELQTNHNOYPLADNPNSTLEELNYKEPLRMTEDSS 53
 Db 1 MKLNQDKHOSPFSSNPKVDKISTDS-----LNKNETDIELQNLNEDCLKMSEYEN 50
 Qy 54 TE-VLDNSTVTDAGTGISIVQGILGWGVYPFAGALTTSYQSFNTINTWPSDADEWKAFMA 112
 Db 51 VEPFVTSITQ-----TSGLTAGKILGTLGIPFAGQAVSILYSPFLGELWPKGKNOWEIENE 106
 Db 113 QVEVLIIKKIEYAKSKALAEQGLLNONFEDVNALNSWKKTPSLRSRSODIRELFS 172
 Qy 107 HVEELINQKISTYARYNKAALTDLGKDLAGVYHDSLESWYG--NRNNTNTRARSVKSQI 163
 Qy 173 QAESHFNRNSMPSPAVSKPEVFLPPTYAQAANANTHLLKDAQVFGREWGSSEDVAFYHR 232
 Qy 164 ALEMFMVQKLPSPAVSGEVPPLPVTAQAAHLILLRASIFGEWGLSSEISTFYNR 223
 Db 233 QLKLTQQYTDHCYCNWYNGVGLNGLRGSTYDAWYKFNFRREMTLVTLIVLFFPDYIRLY 292
 Qy 224 QVERAGDSDHCKWYSGLNNGLRGTAESWYRNQFRDNTMLVLDLVALFPSTQTMV 283
 Db 293 SKGYKTELTRDIFTD-----PIFSLNT-LQEXGPTFLSIENS-IRKPHLFYDLYGIE 342
 Qy 284 PIKTAQLTREVITDAIGTVPHPHSFSTTWNNNAPSFSATEAVVRNPHLDFEQVT 343

RESULT 9

I39814 Insecticidal protein cryVl - *Bacillus thuringiensis*
 C;Species: *Bacillus thuringiensis*
 C;Accession: I39814 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
 C;Date: 19-Jul-1996
 R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
 Appl. Environ. Microbiol. 61, 2402-2407, 1995
 A;Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis* & *tomcodius*.
 A;Reference number: I39814; MUID:95314293; PMID: 7739360
 A;Accession: I39814
 A;Molecule type: DNA
 A;Residues: 1-719 <RES>
 A;Cross-references: GB:L36338; NID:g540281; PID: AAC36999.1; PMID: 9540282
 C;Genetics:

C;Superfamily: parasporal crystal protein
 Query Match Score 1031.5; DB 2; Length 719;
 Best Local Similarity 36.5%; Pred. No. 4.9e-62; Mismatches 232; Indels 63; Gaps 19; Matches 248; Conservative 137; Mismatches 232; Indels 63; Gaps 19;

Qy 1 MNPNNSEHDITI-----KVTPNSELQTNHNOYPLADNPNSTLEELNYKEPLRMTEDSS 53
 Db 1 MKLNQDKHOSPFSSNPKVDKISTDS-----LNKNETDIELQNLNEDCLKMSEYEN 50
 Qy 54 TE-VLDNSTVTDAGTGISIVQGILGWGVYPFAGALTTSYQSFNTINTWPSDADEWKAFMA 112
 Db 51 VEPFVTSITQ-----TSGLTAGKILGTLGIPFAGQAVSILYSPFLGELWPKGKNOWEIENE 106
 Db 113 QVEVLIIKKIEYAKSKALAEQGLLNONFEDVNALNSWKKTPSLRSRSODIRELFS 172
 Qy 107 HVEELINQKISTYARYNKAALTDLGKDLAGVYHDSLESWYG--NRNNTNTRARSVKSQI 163
 Qy 173 QAESHFNRNSMPSPAVSKPEVFLPPTYAQAANANTHLLKDAQVFGREWGSSEDVAFYHR 232
 Db 233 QLKLTQQYTDHCYCNWYNGVGLNGLRGSTYDAWYKFNFRREMTLVTLIVLFFPDYIRLY 292
 Qy 224 QVERAGDSDHCKWYSGLNNGLRGTAESWYRNQFRDNTMLVLDLVALFPSTQTMV 283
 Db 293 SKGYKTELTRDIFTD-----PIFSLNT-LQEXGPTFLSIENS-IRKPHLFYDLYGIE 342
 Qy 284 PIKTAQLTREVITDAIGTVPHPHSFSTTWNNNAPSFSATEAVVRNPHLDFEQVT 343

Qy	343 FHTRLQPGYFGKDSFNYSGNYVTRSSKITSPPYGDKSTEPVQKLSPFDGQKVYR 402	Qy	343 FHTRLQPGYFGKDSFNYSGNYVETRSPGSSKITSPPYGDKSTEPVQKLSPFDGQKVYR 402
Db	344 IYSLIS-RWSNTQYMMNGHKKLEFR-TIGGTNINISTQCSNTNSINPV-TLPFTSRDYR 400	Db	344 IYSLIS-RWSNTQYMMNGHKKLEFR-TIGGTNINISTQCSNTNSINPV-TLPFTSRDYR 400
Qy	403 TIANTDVAAPNGKVKYLGYTKVDFSDQDKNETSTQYDSKRNNGH---VSAQDSIDQ 458	Qy	403 TIANTDVAAPNGKVKYLGYTKVDFSDQDKNETSTQYDSKRNNGH---VSAQDSIDQ 458
Db	401 TESLAGLNFLTQPWN-GVPRVDF---HWKFVTHPIASDNFTYPGYAGIGTQLQDSEN E 455	Db	401 TESLAGLNFLTQPWN-GVPRVDF---HWKFVTHPIASDNFTYPGYAGIGTQLQDSEN E 455
Qy	459 LPPETTDEPLEKAYSHQLYNAEFLMQRDRGTIPPFWTHRSYDFNTIDAEKITQLPV 518	Qy	459 LPPETTDEPLEKAYSHQLYNAEFLMQRDRGTIPPFWTHRSYDFNTIDAEKITQLPV 518
Db	456 LPPEATGQPNYESYSHRLSHIGLISASHYKALV-YSTMTHRSADRNTIEPNSTQIPLV 513	Db	456 LPPEATGQPNYESYSHRLSHIGLISASHYKALV-YSTMTHRSADRNTIEPNSTQIPLV 513
Qy	519 KAYALSSGASIILEGPGFTGQNLLPKESSNSIAFKVTLNSSAALLQRVVRVRYASTNL 578	Qy	519 KAYALSSGASIILEGPGFTGQNLLPKESSNSIAFKVTLNSSAALLQRVVRVRYASTNL 578
Db	514 KAFNLSGGAVVRPGFTGQGDIL-RRNTNGTFCBIRVNIN-PFFAQYRVRVRYASTDL 571	Db	514 KAFNLSGGAVVRPGFTGQGDIL-RRNTNGTFCBIRVNIN-PFFAQYRVRVRYASTDL 571
Qy	579 RLFVQ----NSNNDFLVIVYINKTMNKDDDLTYQTQFDLATTINSMGFSGDKNEELIGAE 632	Qy	579 RLFVQ----NSNNDFLVIVYINKTMNKDDDLTYQTQFDLATTINSMGFSGDKNEELIGAE 632
Db	572 QFHTSINGKAINQGN-----FSATMNRGSEBDLXKTRTVGFTTPSFPLDVQSTFTIGAW 625	Db	572 QFHTSINGKAINQGN-----FSATMNRGSEBDLXKTRTVGFTTPSFPLDVQSTFTIGAW 625
Qy	633 SFVSNEKLYIDKTEFIPVQL 652	Qy	633 SFVSNEKLYIDKTEFIPVQL 652
Db	626 NFSSGNEYVYDRIEFVFPVVE 645	Db	626 NFSSGNEYVYDRIEFVFPVVE 645
RESULT 11			
S00873			
parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis			
N: Alternate names: parasporal crystal protein cryA4			
C: Species: Bacillus thuringiensis			
C: Accession: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004			
C: Accession: S25363			
R:Taylor, R.; Tippett, J.; Gibb, G.; Pike, D.; Jordan, L.; Ely, S.			
Mol. Microbiol. 6:1211-1217, 1992			
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin			
A:Reference number: S23383; PMID:1588820			
A:Accession: S25383			
A:Molecule type: DNA			
A:Residues: 1-719 <TA>			
C:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PIDN:CAA44633.1; PID:940290			
C:Genetics:			
A:Gene: cryA4			
C:Superfamily: parasporal crystal protein			
C:Keywords: delta-endotoxin			
Query Match 32.0%; Score 1091.5; DB 2; Length 719;			
Best Local Similarity 36.5%; Pred. No. 4.0e-62;			
Matches 248; Conservative 137; Mismatches 232; Indels 63; Gaps 19;			
Qy	1 MNPNRSEHDITI-----KVTNSELOTHNHOYPLADNPNSTLEENYKEPLRMTEDSS 53	Qy	1 MNPNRSEHDITI-----KVTNSELOTHNHOYPLADNPNSTLEENYKEPLRMTEDSS 53
Db	1 MKLKNODRQHQSFSNAKVDKISD-----LKNETDIELQINHEDCLKMSYYEN 50	Db	1 MKLKNODRQHQSFSNAKVDKISD-----LKNETDIELQINHEDCLKMSYYEN 50
Qy	54 TE-VLDNSKTVDAVGTGISUVGQOLGVYVPPFGALTSTFYOSPLNTIWPSDADPKWAFMA 112	Qy	54 TE-VLDNSKTVDAVGTGISUVGQOLGVYVPPFGALTSTFYOSPLNTIWPSDADPKWAFMA 112
Db	51 VEPPVSATIQ---TGIGIAKGKLGTVQFQVASLTSFILGEWPKGRQWEMFME 106	Db	51 VEPPVSATIQ---TGIGIAKGKLGTVQFQVASLTSFILGEWPKGRQWEMFME 106
Qy	113 QVEVLIDKKIEEYAKSKKALAELOGLQNFEDTYNALSWKTPSLRSKRSQDRIRELFS 172	Qy	113 QVEVLIDKKIEEYAKSKKALAELOGLQNFEDTYNALSWKTPSLRSKRSQDRIRELFS 172
Db	107 HVEEINQKISTYARNKALDLKGGLDALAVTHDSLSWVG---NRNNTRAVSUQSYI 163	Db	107 HVEEINQKISTYARNKALDLKGGLDALAVTHDSLSWVG---NRNNTRAVSUQSYI 163
Qy	173 QAESHRNSMPSFAVSKPBLFQPTYQAANTHLLKDAQVGEENGYSSEDVAEYHR 232	Qy	173 QAESHRNSMPSFAVSKPBLFQPTYQAANTHLLKDAQVGEENGYSSEDVAEYHR 232
Db	164 ALBLMFVQKLPSAVSAGEVPLPPIYAQANHLILLRDAASFGKEWGLSSSEISITYNR 223	Db	164 ALBLMFVQKLPSAVSAGEVPLPPIYAQANHLILLRDAASFGKEWGLSSSEISITYNR 223
Qy	233 QKLTOOQYTDHCYNWYNGNLNGLRGSTYDAMWTKPNEPREMTLTVLDPFDIRLKG 292	Qy	233 QKLTOOQYTDHCYNWYNGNLNGLRGSTYDAMWTKPNEPREMTLTVLDPFDIRLKG 292
Db	224 QVERAGDYSYHCKWYSTGQNLNRGTAASWRYNQPRDMTLMVLDVALPSYDQMY 283	Db	224 QVERAGDYSYHCKWYSTGQNLNRGTAASWRYNQPRDMTLMVLDVALPSYDQMY 283
Qy	293 SKGVKTTELTDIFTD-----PIFSLNT-LQBYGPPFLSIENS-IRKPHLFDYLOGIE 342	Qy	293 SKGVKTTELTDIFTD-----PIFSLNT-LQBYGPPFLSIENS-IRKPHLFDYLOGIE 342
Db	284 PIKTAQOLREVYTDAIGTVPHPHPSFTSTWNNNAPSFSATEAVYRNPHLDFLEQVT 343	Db	284 PIKTAQOLREVYTDAIGTVPHPHPSFTSTWNNNAPSFSATEAVYRNPHLDFLEQVT 343

Db	279	SAQLTREVYTDIAIGATGVNNVASHMWNNAAPSFSAIEAAIRSPHLLDPEQTLIFS-AS	337	Qy	344	HTRL-QPGYFGKDSFNYWSGNVYETRPSIGSS-KTISPPFYGDKSTEPEVKLSEFDGQK-V	400
Qy	349	PGYFGKDSFNYWSGNVYETRPSIGSS-KTISPPFYGDKSTEPEVKLSEFDGQK-V	406	Db	358	YTSFRONTI - EYYNNGGORLTLYIYGFSFNKYSGVLAGAEDIIPV-----GNDI	409
Db	338	SRSNTRHMTYWRGHTIOSRPIGGGLNTST--HOATNTSINPV-TLRPASRDYRTTSE	393	Qy	401	YRTIANTDVAAMPNGKTYLGVTKUDFSQYDQKNETSOTYDS-KRNNGHVSQAQDSIDOL	459
Qy	407	TDVAAWPNKGKVYL---GTVKVDFSQYDOK-NESTQTDKSRKNGHVSQAQDSIDOLPP	461	Db	410	YRVWW-TIYGRVINS--LLGYNPVTF----YFSNNNTQKTSKPKOFAGGKTTDSGEEL	461
Db	394	AGVLLW -- GIVLEPHGVPVTRFNNTNPQNSIDRGTAINTSQVYESPGIQLQKDSETELPP	450	Qy	460	PPETTDPEPLEKAYSHQNLNYAECPLMORRGT---IPEFTWTHRSDFENTIDAETKTQI	515
Qy	462	ETTDEPLEKAYSHQNLNYAECPLMORRGTIPFETWTHRSDFNTIDAETITOLPVVKAY	521	Db	462	TYEN---YQSYSHRSYTSPEIKSTGGTVLGVUYTEGWTHSSASRNNFYATKSQI	516
Db	451	ETTERPYNEYSRHLSSHIGLIQS - RVNTPEVSMWTHRSADRNTTIGPNRITO1PMVXAS	508	Qy	516	PVVKAYALSGA-SIEBPGFETGGNLLFLKESNSSTAKFKVTLNSMALLORYVRVIRYA	573
Qy	522	ALSSGASLIEEGCFTGDNLFLKESSNSIAKPKVTLNSAAILORTRVRIYASTTNRLRF	581	Db	517	PINKASRTSGGAIVWNPFQGL-YNGGPMLKSGSGSQVNLRVATDKAGASQYRIRYRA	575
Db	509	ELPQGTTVVRGCGFTGFDIL-RRTNTGFGP-IRTVTN-GPLTQRYRIGFYAYSTDDEF	566	Qy	574	S----TTNLRLFVQVNNDFLIVYIYKTMKDDDLTYQFDLATTNS-NMGFSQRNE	626
Qy	582	VONSVN--NDFLVIVYIYKTMKDDDLTYQFDLATTNSNNNGFSGDKNEELLIGAESFVSNE	638	Db	576	SDRAGKFTISSRSPENATYASIAYT-TMSNASYLSTPAYAEGSPINLGIGSSRT	634
Db	567	VSRGGTTVNNNFRFL---RTTNSGDELKXGNGFVRAFFTPTQIQDIINTS1Q3LSGNG	623	Qy	627	LIGAESFTSNEKTYIDKIEFIPV	650
Qy	639	KIYIDKIEFIPV	650	Db	635	FDISITKEAANLYIDRLEFIPV	658
Db	624	EYVIDKIEBIPV	635				
RESULT 13							
					S39326		
					parasporal crystal protein cry9Bal - <i>Bacillus thuringiensis</i>		
					N; Alternative names: delta-endotoxin-related protein; parasporal crystal protein cryX		
					; Species: <i>Bacillus thuringiensis</i>		
					C; Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004		
					C; Accession: S39326		
					R; Shavelley, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepanov, FEBs Lett., 336, 79-82, 1993		
					C; Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from <i>Bacillus thuringiensis</i>		
					A; Reference number: S39326; PMID:8262221		
					A; Status: preliminary		
					A; Accession: S39326		
					A; Molecule type: DNA		
					A; Residue: 1-1154 - SHE		
					A; Cross-references: UNIPROT:045745; EMBL:X75019		
					C; Superfamily: Parasporal crystal protein		
					C; Keywords: delta-endotoxin		
RESULT 12							
	140589	parasporal crystal protein cry8Cai - <i>Bacillus thuringiensis</i>			Query Match Score 963.5 ; DB 2; Length 1154;		
		N; Alternative names: parasporal crystal protein cryIII			Best Local Similarity 33.3% ; Pred. No. 1.5e-53;		
		C; Species: <i>Bacillus thuringiensis</i>			Mismatches 243; Indels 51; Gaps 16;		
		C; Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004			Matches 214; Conservative 135; Mismatches 214;		
		C; Accession: I40589			Query Match Score 963.5 ; DB 2; Length 1154;		
		C; Authors: R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano, Curr. Microbiol. 28, 15-19, 1994			Best Local Similarity 33.3% ; Pred. No. 1.5e-53;		
		A; Title: Cloning, heterologous expression, and localization of a novel crystal protein 9			Mismatches 214; Conservative 135; Mismatches 243; Indels 51; Gaps 16;		
		A; Reference number: I40589; PMID:7784305			Query Match Score 963.5 ; DB 2; Length 1154;		
		A; Status: preliminary; translated from GB/EMBL/DDBJ			Best Local Similarity 33.3% ; Pred. No. 1.5e-53;		
		A; Molecule type: DNA			Mismatches 214; Conservative 135; Mismatches 243; Indels 51; Gaps 16;		
		A; Cross-references: UNIPROT:Q45706; EMBL:U04366; NID:9532523; PID:95325			Query Match Score 963.5 ; DB 2; Length 1154;		
		C; Superfamily: parasporal crystal protein			Best Local Similarity 33.3% ; Pred. No. 1.5e-53;		
		C; Keywords: delta-endotoxin			Mismatches 214; Conservative 135; Mismatches 243; Indels 51; Gaps 16;		
Qy	1	MYPNIRSEHDITKTPNSLQTNENQYPLADNPNSTLPELNQYKFLRMTEEDSSTEVIDLNS	60	Qy	41	NYKEFLRMTE-DSSTEVLDNSTVKAQVDTGTSVYQCLQGVPPAGALTFSYQOSFLNTI	99
Db	1	MSPNQNKEYTIDALSPTYSDSNTRYPANDQNTLQMNQYKDLKNTESTNAELSRNP	60	Db	29	SYKDYKMSBEDIDSYEINPONVRGQLDTQVAVVQALGGPGVGLTGFLSLFGFL	88
Qy	61	---	---	Qy	100	WPS-DADPKWAKMAQEVLIDKKIEFYAKSKALAEGLQGONNFEDYVNAINSWKCTPLSL	158
Db	121	TVKDQAVGTGIVSUGQILGVNVGPAGALTSFYQSPFLNTIWP5-DADPKWAKMAQE	115	Db	89	WPSNDQAVWEAFQMEQNLBEQTRISQVTRALDDGIONYINOLIAALKEWEPNGV	148
Qy	61	GTFISQDQAVGTGIVSUGQILGVNVGPAGALTSFYQSPFLNTIWP5-DADPKWAKMAQE	115	Qy	159	RSKRSDQIRELFQSQESHFANMSPEF--AVSKFEVLFLPTYQAQANTHLLKDAOV	214
Db	120	---	---	Db	149	RA---IUVLQRFEIILHALFVSSMPFGSGFSQRSQEQAQVLAQVHLLDAEK	204
Qy	61	SHFRNSMPSFASVSKFELVFLPTYQAQANTHLLKDAQYFEEGVYSSSDVAEFYHRQLK	235	Qy	205	YQARWKQRESQIGNYFNEQLOTRTRDYNQHNAVNGLAGLRGSAESWVQHORRE	264
Db	116	VLIDKKEETAKSALAEGLQNLQNNFEDYVNAINSWKCTPLSLRSKSCDRIBELSOAE	175	Db	274	TLTVDLIVLFPFYDYLRYSKVCKTLETRDIFTDP-----ISSLNTLQGYGP	320
Qy	116	---	---	Qy	265	TUMAMDLALFPYNTNTRYPIAVNPQTREYTDPLGPVSESSLPELRLCLRQTSAM	324
Db	121	BLIDQKILDSVRSRAIDLANSRIAVEYQNALDEDWRNP--HSTRSALVAKERGNAE	177	Db	321	TELSIENS-IRKPHLFQDLYQOLIEFHTRPQYFGKDSFNTYMSGNTYVETRPIGSSITIS	379
Qy	117	---	---	Qy	325	TFSNLNENAISSPHLFDTINNLMYGSVHLTNQLEGWIGHSYTSSILLASGPITVLR	384
Db	120	YTERAYSDHCVYQVAGNKURGTGAXQWDFNMRNFRERMYAVLDPVNPYDARYIPL	297	Db	298	TNAELTRTIEDPFIPLSINTLQE-----YQ-----PTFLSIENSIRKPHLFQDLYQOLIEFHTRPQYFGKDSFNTYMSGNTYVETRPIGSSITIS	357

380 PFXGDKSTPQVQLSFDGQQVKYR-TIANTDVAAMPNGKVLYGLGVTKVDSQYDDQKNETS 437
 385 RNYG-SITIVNNTSFNDRDYQINTRSSTGL-GFONADLF-GITRAQF-----YV 432
 388 TQTYDSKRNRGHVSAQ-PDSIDQLPETTDEPLEKAYSHQNLNAYAECFL-----YV 432
 438 GGTTSVTQNRNALTCEQNNSIDESLSDNEPISRSYSHRLSHITSYLHRLVLTIDGININY 492
 488 RTGTPFFFTWTHRSDFFTNTDAEKITOLQVLPVKAIALSSGASITIEGGFTG 538
 493 SGNLPLTYVTHRDVLNTTADRTQOLLVKSPEIAPTTVURGPFFGDDIL-RRTGV 551
 548 NSIAKFKTVLNSAALLQRYVRVIRYASTTNLRFLVQNSNDELVYIYNTMANKDDLTYQ 607
 552 GTFGTIVR-TTAPtQTRRIRFPAStTFLFCIGIRVGRQVNYFDFGRTMARGDELYR E 610
 608 TFDLATTNSNMGFSGDKNRELLIGAESFVSNEMEKYIYDKEFIPV 650
 611 SPATREFTDENPFRQPOELISVFANAFASSQEVYFDRLEIIPV 653

RESULT 14

JC7140

protoxin - Bacillus thuringiensis

C:Alternate names: cry1C protein

C:Species: Bacillus thuringiensis

C:Accession: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

R;Chrisirov, N.K.; Imaiishi, H.; Ohkawa, H.

Biosci. Biotechnol. Biochem. 63, 1433-1444, 1999

A;Title: Green-tissue-specific expression of a reconstructed cry1C gene encoding the actuator litura

A;Reference number: JC7140; MUID:99430790; PMID:10501003

A;Molecule type: DNA

A;Residues: 1-655 <CHR>

A;Cross-references: EMBL:X96682

C;Genetics:

A;Gene: cry1C

C;Superfamily: parasporal crystal protein

Query Match Score 934.5; DB 2; Length 655;

Best Local Similarity 36.3%; Pred. No. 4.7e-52; Matches 242; Conservative 103; Mismatches 227; Indels 95; Gaps 27;

QV 21 QTHHNQ--YPLADNPNSTLEELNPKFLRMTEDSSTEVDLN--STYKDAGTGIVSIVG 74
 Db 3 ENNONQC1PYNCUSNPSEVL-----LDGERISTGNNSIDSLSLV- 42QV 75 QILGVGVGVFFAGALTSFVQSFLNTIWPFDADPKFAFMQVEVILDKKIEYAKSKALAE 134
 Db 43 QFLVSNPVGGGFLVGLIDFWNGIVGPSO--WDAFLVQIEQLINERIAEFARNAAANL 99QV 135 QGLONNFEDYNALNWSKKTPLSLRSKESQRDRFLFQABSHFRNSMSPFAVSKFEVIL 194
 Db 100 EGLGNNFNIVYEAFKEWEDP--NNPATRTRVIDRFLDGLHLERDPSRISGFEPV 156QV 195 LPTYAQANTHLLLKDQVGEEMGSSEDVAEYHRQLKLTOQYDHCVNPNVNGLNG 254
 Db 157 LSYYAQANLHAILRDSVIFGERWGLTINVNENYNLIRHDEADHCANTYNRLGLNN 216QV 255 LRGSTYDAWKENFRERREMTLTVLDLIVPFYDIRLYSKGVKTLETRDIDTPIFPSLN- 313
 Db 217 LPKSTYQDWTINRLRDLTTLVLDIAAFFPNTLRLQQPWNAPPENLRGVSEG 330QV 314 TLOBYG--PTFLSIENS-TRKPHFLDYLGIEPHTRLOGFYFKDSFNYWSGNYVEPRPS 370
 Db 277 QLSVQAQLPTFNMESSIRPNPHFLDILNLTT-----DWFSVGRNFYWGGRVIS-S 330QV 371 IGSSKTTITSPPFG-DKSTEPVQKLSDGQKVYRTIANTDV---AWPNKGKVYL-GVTKV 424
 Db 331 LIGGGNTTSPYGVGREANQEPFRSFTENG-PVFRTLSNPTLRLQQPWNAPPFLRGVSEG 389

QV 425 DFGQYDDOKNETSTQTYDSKRNRGHVSAQDSIDQLPETTDEPLEKAYSHQNLNAYECFLM 484

RESULT 15

S00944

parasporal crystal protein cry1Ca1 - Bacillus thuringiensis (strain entomocidus 60-5)

C:Species: Bacillus thuringiensis

C:Accession: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

R;Honee, G.; van der Salm, T.; Visser, B.

Nucleic Acids Res 16, 6240, 1988

A;Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis subs

A;Reference number: S00944; MUID:88269380; PMID:3399402

A;Accession: S00944

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-1189 <HON>

A;Cross-references: UNIPROT:P05518; EMBL:X07518; PIDN:940293; PIDN:CAA30396.1; PID:940294

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

C;Keywords: delta-endotoxin

Query Match Score 926.5; DB 2; Length 1189;
 Best Local Similarity 36.1%; Pred. No. 3.7e-51; Matches 241; Conservative 103; Mismatches 228; Indels 95; Gaps 27;
 QV 21 QTTHHNQ--YPLADNPNSTLEELNPKFLRMTEDSSTEVDLN--STYKDAGTGIVSIVG 74
 Db 3 ENNONQC1PYNCUSNPSEVL-----LDGERISTGNNSIDSLSLV- 42
 QV 75 QILGVGVGVFFAGALTSFVQSFLNTIWPFDADPKFAFMQVEVILDKKIEYAKSKALAE 134
 Db 43 QFLVSNPVGGGFLVGLIDFWNGIVGPSO--WDAFLVQIEQLINERIAEFARNAAANL 99
 QV 135 QGLONNFEDYNALNWSKKTPLSLRSKESQRDRFLFQABSHFRNSMSPFAVSKFEVIL 194
 Db 100 EGLGNNFNIVYEAFKEWEDP--NNPATRTRVIDRFLDGLHLERDPSRISGFEPV 156
 QV 195 LPTYAQANTHLLLKDQVGEEMGSSEDVAEYHRQLKLTOQYDHCVNPNVNGLNG 254
 Db 157 LSYYAQANLHAILRDSVIFGERWGLTINVNENYNLIRHDEADHCANTYNRLGLNN 216
 QV 255 LRGSTYDAWKENFRERREMTLTVLDLIVPFYDIRLYSKGVKTLETRDIDTPIFPSLN- 313
 Db 217 LPKSTYQDWTINRLRDLTTLVLDIAAFFPNTLRLQQPWNAPPFLRGVSEG 330
 QV 314 TLOBYG--PTFLSIENS-TRKPHFLDYLGIEPHTRLOGFYFKDSFNYWSGNYVEPRPS 370
 Db 277 QLSVQAQLPTFNMESSIRPNPHFLDILNLTT-----DWFSVGRNFYWGGRVIS-S 330
 QV 371 IGSSKTTITSPPFG-DKSTEPVQKLSDGQKVYRTIANTDV---AWPNKGKVYL-GVTKV 424
 Db 331 LIGGGNTTSPYGVGREANQEPFRSFTENG-PVFRTLSNPTLRLQQPWNAPPFLRGVSEG 389
 QV 425 DFGQYDDOKNETSTQTYDSKRNRGHVSAQDSIDQLPETTDEPLEKAYSHQNLNAYECFLM 484

Db	390	EFS-----TPTNSFTY--RGRGTV--DSLTELPPEDNSVPREGYSHRLCHA---TF	434	Db	390	EFS-----TPTNSFTY--RGRGTV--DSLTELPPEDNSVPREGYSHRLCHA---TF	434
Qy	485	QDRRGITPFF-----FTWTRSDPENTIAEKTITOLPVKAYALSGASITIEGPFGTG	538	Qy	485	QDRRGITPFF-----FTWTRSDPENTIAEKTITOLPVKAYALSGASITIEGPFGTG	538
Db	435	VQRSGT-PFLTGTVVSWTDATLNTIDPERINQIPLYKGFRWGGTSVTSVSPGFCC	493	Db	435	VQRSGT-PFLTGTVVSWTDATLNTIDPERINQIPLYKGFRWGGTSVTSVSPGFCC	493
Qy	539	NLLFLKESSNSIAKEPKVTLNSAALLQRYRIRYASTTNURLFV-----QNSNN	587	Qy	539	NLLFLKESSNSIAKEPKVTLNSAALLQRYRIRYASTTNURLFV-----QNSNN	587
Db	494	DIL-RNRTGDFVSQYNINS-PITORYRIRYASRDARTVLTGAASITGVGGQSVN	551	Db	494	DIL-RNRTGDFVSQYNINS-PITORYRIRYASRDARTVLTGAASITGVGGQSVN	551
Qy	588	DLVLYINKTMKDDDTYQFDLATNSNGFS-----GDKNELLIGAESFVNNEKLY	641	Qy	588	DLVLYINKTMKDDDTYQFDLATNSNGFS-----GDKNELLIGAESFVNNEKLY	641
Db	552	-MPLQTKMEIGENITSRTERTYTDTSNPFSFRANPDIGCISEQPLFGGS-ISSGELY	606	Db	552	-MPLQTKMEIGENITSRTERTYTDTSNPFSFRANPDIGCISEQPLFGGS-ISSGELY	606
Qy	642	IDKIEFI 648	648	Qy	642	IDKIEFI 648	648
Db	607	IDKIEII 613	607	Db	607	IDKIEII 613	607
RESULT 17							
	S02134	parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai IC1)					
	N;Alternate names:	delta-endotoxin					
	C;Species:	Bacillus thuringiensis					
	C;Date:	07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004					
	C;Accession:	S04181					
	R;Haider,M.Z.; Ellar,D.J.						
	Mol. Microbiol. 3, 229-238, 1989						
	A;Title: Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera frugiperda delta-endotoxin gene						
	A;Reference number: S04181; PMID:89343627; PMID:2548660						
	A;Accession: S04181						
	A;Molecule type: DNA						
	A;Residues: 1-823 <SAN>						
	A;Cross-references: UNIPROT:P05518; EMBL:X13620; NID:940355; PIDN:CAA31951.1; PID:940356						
	C;Genetics:						
	A;Gene: bta						
	C;Superfamily: parasporal crystal protein						
	C;Keywords: delta-endotoxin						
RESULT 16							
	S04181	parasporal crystal protein - Bacillus thuringiensis (strain aizawai 7.29) (Fragment)					
	N;Alternate names:	delt-endotoxin					
	C;Species:	Bacillus thuringiensis					
	C;Date:	07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004					
	C;Accession:	S04181					
	R;Haider,M.Z.; Ellar,D.J.						
	Mol. Microbiol. 3, 229-238, 1989						
	A;Title: Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera frugiperda delta-endotoxin gene						
	A;Reference number: S04181; PMID:89343627; PMID:2548660						
	A;Accession: S04181						
	A;Molecule type: DNA						
	A;Residues: 1-823 <SAN>						
	A;Cross-references: UNIPROT:P05518; EMBL:X13620; NID:940355; PIDN:CAA31951.1; PID:940356						
	C;Genetics:						
	A;Gene: bta						
	C;Superfamily: parasporal crystal protein						
	C;Keywords: delta-endotoxin						
Query Match 26.6%							
Qy	21	QTNHENQ---YPLADNPNSTLEINYKEPLRMTEDSSTEVLDN---STVKDAVGTGTSVVG	74	Qy	21	QTNHENQ---YPLADNPNSTLEINYKEPLRMTEDSSTEVLDN---STVKDAVGTGTSVVG	74
Db	3	ENNONQCFCYNCISNPNEVIL-----GERISTGNSSDISLSLV-	42	Db	3	ENNONQCFCYNCISNPNEVIL-----GERISTGNSSDISLSLV-	42
Qy	75	QILGVGVGYPFAGALTSEFYQSFLNTIWPSPDADPKAFMAQVEVLI	134	Qy	75	QILGVGVGYPFAGALTSEFYQSFLNTIWPSPDADPKAFMAQVEVLI	134
Db	43	QFLVSNFVGGFLVGLIDEFWGTVGPSSO---WDAFLVQEQLINERIAFARNAIAANL	99	Db	43	QFLVSNFVGGFLVGLIDEFWGTVGPSSO---WDAFLVQEQLINERIAFARNAIAANL	99
Qy	135	QGLONNPEKYVNLNSWKKTPSLRSKESODRRELQFQAEHSFRNEMPSFAVSKPEVLF	194	Qy	135	QGLONNPEKYVNLNSWKKTPSLRSKESODRRELQFQAEHSFRNEMPSFAVSKPEVLF	194
Db	100	EGLNENNFTNVEAKEYEWEDDP---NNPATRTRVDRFLGILERDPIFLNPIFLNPI	156	Db	100	EGLNENNFTNVEAKEYEWEDDP---NNPATRTRVDRFLGILERDPIFLNPIFLNPI	156
Qy	195	LPTYAQAAANTHLILKDAVQFGEWGWYSSVEDVAEFPYRQLKLQTQYDTHCNWNYGLNG	254	Qy	195	LPTYAQAAANTHLILKDAVQFGEWGWYSSVEDVAEFPYRQLKLQTQYDTHCNWNYGLNG	254
Db	157	LSVYQAQANLHLAIRDSVTFGERWLTTINVNENYNFLRHDAYADCACTYRNGLNN	216	Db	157	LSVYQAQANLHLAIRDSVTFGERWLTTINVNENYNFLRHDAYADCACTYRNGLNN	216
Qy	255	LRGSTYDAWVYKFNFRFREMLTVLDLIVPFPYDILYNSKGVKTELDIFDPFLNPI	313	Qy	255	LRGSTYDAWVYKFNFRFREMLTVLDLIVPFPYDILYNSKGVKTELDIFDPFLNPI	313
Db	217	LPKSTYQDNNTYNRRLDTLTVLDAIAFPNTYDNRRFIQPGQLTREVYDPLINFP	276	Db	217	LPKSTYQDNNTYNRRLDTLTVLDAIAFPNTYDNRRFIQPGQLTREVYDPLINFP	276
Qy	314	TLOQEYG-PPIFLSIENS-TRKPHLFDYDQYEFTRLQGYGFDGSFENWGNVYETRPS	370	Qy	314	TLOQEYG-PPIFLSIENS-TRKPHLFDYDQYEFTRLQGYGFDGSFENWGNVYETRPS	370
Db	277	QLQSYAQLPNTVWMESSAARNPHLFDILNNLTIPT---DWFSYGRNFYWGHHRVIS	330	Db	277	QLQSYAQLPNTVWMESSAARNPHLFDILNNLTIPT---DWFSYGRNFYWGHHRVIS	330
Qy	371	IGSSKTTSPFYG-DKSTBFVQKLSFDQGKVYRT-IANTDVAAWPNGKRYV--GVTKV	424	Qy	371	IGSSKTTSPFYG-DKSTBFVQKLSFDQGKVYRT-IANTDVAAWPNGKRYV--GVTKV	424
Db	331	LIGGENITSPYGRGANQEPRSSFTFNG-PVFRTLSIPTLRLQQCPHHRFLRGGGV	389	Db	331	LIGGENITSPYGRGANQEPRSSFTFNG-PVFRTLSIPTLRLQQCPHHRFLRGGGV	389
Qy	425	DFSQYDDQKNETSTQTYDSKRNNGHVSAQDSIDQPPTDEPLEKAYSHOLNYAECFLM	484	Qy	425	DFSQYDDQKNETSTQTYDSKRNNGHVSAQDSIDQPPTDEPLEKAYSHOLNYAECFLM	484
Db	390	EFS-----TPTNSFTY--RGRGTV--DSLTELPPEDNSVPREGYSHRLCHA---TF	434	Db	390	EFS-----TPTNSFTY--RGRGTV--DSLTELPPEDNSVPREGYSHRLCHA---TF	434
Qy	485	QDRRGITPFF-----FTWTRSDPENTIAEKTITOLPVKAYALSGASITIEGPFGTG	538	Qy	485	QDRRGITPFF-----FTWTRSDPENTIAEKTITOLPVKAYALSGASITIEGPFGTG	538
Db	435	VQRSGT-PFLTGTVVSWTDATLNTIDPERINQIPLYKGFRWGGTSVTSVSPGFCC	493	Db	435	VQRSGT-PFLTGTVVSWTDATLNTIDPERINQIPLYKGFRWGGTSVTSVSPGFCC	493
Qy	539	NLLFLKESSNSIAKEPKVTLNSAALLQRYRIRYASTTNURLFV-----QNSNN	587	Qy	539	NLLFLKESSNSIAKEPKVTLNSAALLQRYRIRYASTTNURLFV-----QNSNN	587
Db	494	DIL-RNRTGDFVSQYNINS-PITORYRIRYASRDARTVLTGAASITGVGGQSVN	551	Db	494	DIL-RNRTGDFVSQYNINS-PITORYRIRYASRDARTVLTGAASITGVGGQSVN	551
Qy	588	DLVLYINKTMKDDDTYQFDLATNSNGFS-----GDKNELLIGAESFVNNEKLY	641	Qy	588	DLVLYINKTMKDDDTYQFDLATNSNGFS-----GDKNELLIGAESFVNNEKLY	641
Db	552	-MPLQTKMEIGENITSRTERTYTDTSNPFSFRANPDIGCISEQPLFGGS-ISSGELY	606	Db	552	-MPLQTKMEIGENITSRTERTYTDTSNPFSFRANPDIGCISEQPLFGGS-ISSGELY	606
Qy	642	IDKIEFI 648	648	Qy	642	IDKIEFI 648	648
Db	607	IDKIEII 613	607	Db	607	IDKIEII 613	607

Qy	321 TP----LSIENSIRKPHLFIDYLQGIEFHTRLQPGYFGKUDSNTWSGNVTETRPSIGSSRT 376	Db	333 FTFPLUYGTGMNAAQFQRIVAQLGCGGVYRTLSS-----LYRPFNIGINNNQLSVL 383
Db	279 SFRGSAQLEGSISSPHLMDILNSITYTDahrgey----YWSGHQIMASPVGFSGPE 332	Qy	430 DDQKNETSTOT-----YDSKRANGHVSQDSDTDLQLPPTTDEPLEKAYSHOLNABCFL 483
Qy	377 ITSPFYGDK-STEPVQKLSD-FGKVYRTANTDVAAPNGKTY----LGVTKVDFFSCY 429	Db	384 DGTEFAYGTSNLPSAVY---RISGTV---DSLDDEIPQNNTVPPRGFSHRLSHVSMFR 437
Db	333 FTFLUYGTGMNAAPQQRIVAQLGCGVYRTLSS-----LYRPFNIGINNNQLSVL 383	Qy	484 MQDRGTI-----PFTFATHRSDFNTIDAEKITQLPVKAYALSSGASITEGGFTGG 538
Qy	430 DDQKNETSTOT-----YDSKRANGHVSQDSDTDLQLPPTTDEPLEKAYSHOLNABCFL 483	Db	438 SGFNSNSVIIIRAPMSWTHSAEFPNNIPISSQTQIPLTGSTNLGSVVKCPGFTGG 497
Db	384 DGTEFAYGTSNLPSAVY---RISGTV---DSLDDEIPQNNTVPPRGFSHRLSHVSMFR 437	Qy	539 NLLFLKESSNSIAKFKVTLNSAALLQYRVRVIRYASTTNLRLF-----NSNNDFLVI 592
Qy	484 MQDRGTI-----PFTFATHRSDFNTIDAEKITQLPVKAYALSSGASITEGGFTGG 538	Db	498 DIL-RRTSGQISTLRVNI-TAPLSQRVIRYASTTNLQFHTSIDGRPINQGN-----550
Db	438 SGFNSNSVIIIRAPMSWTHSAEFPNNIPISSQTQIPLTGSTNLGSVVKCPGFTGG 497	Qy	593 YINKTMNKDDDTYTQFDLATTNSMGFDKNEELIGAESFSVNEKYIDKIEFIPVQL 652
Qy	539 NLLFLKESSNSIAKFKVTLNSAALLQYRVRVIRYASTTNLRLF-----VONSNNDFLVI 592	Db	551 -FSATMSSSNLQSGSFRTVGFTIPFNFSNGNSVFTLSAHVFNSGNEYIDRTEPVPAEV 609
Db	498 DIL-RRTSGQISTLRVNI-TAPLSQRVIRYASTTNLQFHTSIDGRPINQGN-----550	Qy	593 YINKTMNKDDDTYTQFDLATTNSMGFDKNEELIGAESFSVNEKYIDKIEFIPVQL 652
Qy	551 -FSATMSSSNLQSGSFRTVGFTIPFNFSNGNSVFTLSAHVFNSGNEYIDRTEPVPAEV 609	RESULT 19	parasporal crystal protein cry1Ab3 - Bacillus thuringiensis
Db	A26513 parasporal crystal protein - Bacillus thuringiensis (strain aizawai)	JD0002	# Alternative names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal protein
Cross-references:	Bacillus thuringiensis	C:Species:	Bacillus thuringiensis
Date:	11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 09-Jul-2004	C:Accession:	A90025; A91560; A90955; S14555; A6461; A24172; A29043; JD0002
Accession:	A26513	C:Date:	28-Dec-1987 #text_change 09-Jul-2004
Source:	Bacillus thuringiensis	C:Sequence revision:	A90025; A91560; A90955; S14555; A6461; A24172; A29043; JD0002
Author:	R;Kondo, S.; Tamura, N.; Kunitate, A.; Akashi, A.; Ohmori, I.	Author:	R;Kondo, S.; Tamura, N.; Kunitate, A.; Akashi, A.; Ohmori, I.
Journal:	Agric. Biol. Chem. 51, 455-463, 1987	Journal:	Agric. Biol. Chem. 51, 455-463, 1987
Page:	Gene 48, 109-118, 1986	Page:	Gene 48, 109-118, 1986
Abstract:	The hyper-variable region in the genes coding for two insecticidal delta-endotoxin genes from A26513 was cloned and nucleotide sequencing of two insecticidal delta-endotoxin genes from A26513 was performed.	Abstract:	The hyper-variable region in the genes coding for two insecticidal delta-endotoxin genes from A26513 was cloned and nucleotide sequencing of two insecticidal delta-endotoxin genes from A26513 was performed.
Reference number:	A90025	Reference number:	A90025
Molecule type:	mRNA	Molecule type:	mRNA
Residues:	1-1155 <KON>	Residues:	1-1155 <GET>
Cross-references:	UNIPROT:P06578	Cross-references:	GB: M15271; NID:9143123; PIDN:AAA22561.1; PID:9143124
Experimental source:	subsp. kurstaki	Experimental source:	subsp. kurstaki
Author:	R.Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.	Author:	R.Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
Journal:	DNA 5, 305-314, 1986	Journal:	DNA 5, 305-314, 1986
Page:	A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from A26513	Page:	A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from A26513
Abstract:	The hyper-variable region in the genes coding for two insecticidal delta-endotoxin genes from A26513 was cloned and nucleotide sequencing of two insecticidal delta-endotoxin genes from A26513 was performed.	Abstract:	The hyper-variable region in the genes coding for two insecticidal delta-endotoxin genes from A26513 was cloned and nucleotide sequencing of two insecticidal delta-endotoxin genes from A26513 was performed.
Reference number:	A91560; MUID:87163505; PMID:3557124	Reference number:	A91560; MUID:87163505; PMID:3557124
Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155	Residues:	1-1155
Cross-references:	GB: M15271; NID:9143123; PIDN:AAA22561.1; PID:9143124	Cross-references:	GB: M15271; NID:9143123; PIDN:AAA22561.1; PID:9143124
Experimental source:	subsp. kurstaki	Experimental source:	subsp. kurstaki
Author:	R.Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.	Author:	R.Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
Journal:	DNA 5, 305-314, 1986	Journal:	DNA 5, 305-314, 1986
Page:	A;Title: Bacillus thuringiensis entomocidal protoxin sequence and gene product analysis	Page:	A;Title: Bacillus thuringiensis entomocidal protoxin sequence and gene product analysis
Abstract:	The complete nucleotide sequence of a cry1Ab3 protoxin from A26513 was determined.	Abstract:	The complete nucleotide sequence of a cry1Ab3 protoxin from A26513 was determined.
Reference number:	A90955	Reference number:	A90955
Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155 <WAB>	Residues:	1-1155 <WAB>
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Chak, K.F.; Jen, J.C.	Author:	R.Chak, K.F.; Jen, J.C.
Journal:	EMLB Data Library, October 1990	Journal:	EMLB Data Library, October 1990
Page:	Submitted to the EMBL Data Library, October 1990	Page:	Submitted to the EMBL Data Library, October 1990
Abstract:	Complete nucleotide sequence and expression in Escherichia coli of a cry1Ab3 protoxin from A26513.	Abstract:	Complete nucleotide sequence and expression in Escherichia coli of a cry1Ab3 protoxin from A26513.
Reference number:	S14555	Reference number:	S14555
Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155	Residues:	1-1155
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.	Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.
Journal:	Biochem. 161, 273-280, 1986	Journal:	Biochem. 161, 273-280, 1986
Page:	A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuringiensis	Page:	A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuringiensis
Abstract:	This toxin is lethal to the larvae of lepidopterans and dipterans.	Abstract:	This toxin is lethal to the larvae of lepidopterans and dipterans.
Reference number:	A26461; MUID:87054026; PMID:3023091	Reference number:	A26461; MUID:87054026; PMID:3023091
Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155 <CHA>	Residues:	1-1155 <CHA>
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.	Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.
Journal:	Biochem. 161, 273-280, 1986	Journal:	Biochem. 161, 273-280, 1986
Page:	A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuringiensis	Page:	A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuringiensis
Abstract:	This toxin is lethal to the larvae of lepidopterans and dipterans.	Abstract:	This toxin is lethal to the larvae of lepidopterans and dipterans.
Reference number:	A26461; MUID:87054026; PMID:3023091	Reference number:	A26461; MUID:87054026; PMID:3023091
Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155 <WAB>	Residues:	1-1155 <WAB>
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Chak, K.F.; Jen, J.C.	Author:	R.Chak, K.F.; Jen, J.C.
Journal:	EMLB Data Library, October 1990	Journal:	EMLB Data Library, October 1990
Page:	Submitted to the EMBL Data Library, October 1990	Page:	Submitted to the EMBL Data Library, October 1990
Abstract:	Complete nucleotide sequence and expression in Escherichia coli of a cry1Ab3 protoxin from A26513.	Abstract:	Complete nucleotide sequence and expression in Escherichia coli of a cry1Ab3 protoxin from A26513.
Reference number:	S14555	Reference number:	S14555
Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155	Residues:	1-1155
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.	Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.
Journal:	Biochem. 161, 273-280, 1986	Journal:	Biochem. 161, 273-280, 1986
Page:	A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuringiensis	Page:	A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuringiensis
Abstract:	This toxin is lethal to the larvae of lepidopterans and dipterans.	Abstract:	This toxin is lethal to the larvae of lepidopterans and dipterans.
Reference number:	A26461; MUID:87054026; PMID:3023091	Reference number:	A26461; MUID:87054026; PMID:3023091
Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155 <CHA>	Residues:	1-1155 <CHA>
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
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Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155 <WAB>	Residues:	1-1155 <WAB>
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Chak, K.F.; Jen, J.C.	Author:	R.Chak, K.F.; Jen, J.C.
Journal:	EMLB Data Library, October 1990	Journal:	EMLB Data Library, October 1990
Page:	Submitted to the EMBL Data Library, October 1990	Page:	Submitted to the EMBL Data Library, October 1990
Abstract:	Complete nucleotide sequence and expression in Escherichia coli of a cry1Ab3 protoxin from A26513.	Abstract:	Complete nucleotide sequence and expression in Escherichia coli of a cry1Ab3 protoxin from A26513.
Reference number:	S14555	Reference number:	S14555
Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155	Residues:	1-1155
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.	Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.
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Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155 <CHA>	Residues:	1-1155 <CHA>
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.	Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.
Journal:	Biochem. 161, 273-280, 1986	Journal:	Biochem. 161, 273-280, 1986
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Residues:	1-1155 <WAB>	Residues:	1-1155 <WAB>
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
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Author:	R.Chak, K.F.; Jen, J.C.	Author:	R.Chak, K.F.; Jen, J.C.
Journal:	EMLB Data Library, October 1990	Journal:	EMLB Data Library, October 1990
Page:	Submitted to the EMBL Data Library, October 1990	Page:	Submitted to the EMBL Data Library, October 1990
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Residues:	1-1155	Residues:	1-1155
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
Experimental source:	subsp. berliner	Experimental source:	subsp. berliner
Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.	Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.
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Molecule type:	DNA	Molecule type:	DNA
Residues:	1-1155 <CHA>	Residues:	1-1155 <CHA>
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
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Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.	Author:	R.Hofte, H.; de Gruve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerckhove, J.
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Residues:	1-1155	Residues:	1-1155
Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273	Cross-references:	ENBL:X54939; NID:940272; PIDN:CAA38701.1; PID:940273
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Reference number:	A26461; MUID:87054026; PMID:3023091	Reference number:	

C;Genetics:
A;Gene: cry-1-2, br2
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
C;Product: toxic peptide #status predicted <txp>
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Best Local Similarity 33.3%; Pred. No. 1.9e-19;
Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;

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Db 3 NNPIN-ECPY---NCLSNPEVEVIGGERIE----AGALTSFYOSFINTIW----PSDADPKMAQEVNLIDKIEEYAKSKALAELQGLNN 140
Qy 85 AGALTSFYOSFINTIW----PSDADPKMAQEVNLIDKIEEYAKSKALAELQGLNN 140
Db 54 AG---PVLGLVLDIINGIFGPQS---WDAFLVQEQLINQRLEPANOQASRLEGLSNL 106
Qy 141 FEDVNALNSWKKTPPLSLRSKRSODRTRFLSQASHEFRNSMPSFAVSKFEVFLPTIAQ 200
Db 107 YQYAEASPREWEADPTN-PALREEMRIO-FNDMNSALTAFLPAVQNYQPLLSVYVQ 163
Qy 201 AANTHLLKLKDAAQVGEENGYSSEDVAEYFHROLKLTOQYTDFCHCVNWNNGLRLRSSTY 260
Db 164 AANHLHSVLRDVSFGQMRGFQDATTINSRYNDLTLRIGNYDHAVRNTGQSRVWGPDS 223
Qy 141 FEDVNALNSWKKTPPLSLRSKRSODRTRFLSQASHEFRNSMPSFAVSKFEVFLPTIAQ 200
Db 107 YQYAEASPREWEADPTN-PALREEMRIO-FNDMNSALTAFLPAVQNYQPLLSVYVQ 163
Qy 201 AANTHLLKLKDAAQVGEENGYSSEDVAEYFHROLKLTOQYTDFCHCVNWNNGLRLRSSTY 260
Db 164 AANHLHSVLRDVSFGQMRGFQDATTINSRYNDLTLRIGNYDHAVRNTGQSRVWGPDS 223
Qy 261 DAWKFNFRERRENTLTVDLIVLFPFDYRILYSKGKVTELTDRDPIFSLNTLQEQYGP 320
Db 224 RDWTRYNQNRERRELTVLDPFQDFTVLPNTDSRTYPIRTVSQLTRELYTNPV----LENFDG 278
Qy 321 TF----LSLENSIRKPHLFDYLOGIEFTRLQPEYFKDSENFTWSGNVETRPSIGSSKT 376
Db 279 SFRGSAQIGLEGSIKSPLHMDLNSITVDTAHTWVNTGTLERWGPD 223
Qy 377 ITSPFYGDK-STEVPQKLSFD-GOKVYRINTDVAWNGKVY----LGVTKVDIFSGY 429
Db 333 FTFFPXYGMNAAPQRIYAQLGQSYVRLSST-----LYRPPFMGINNNQQLSVL 383
Qy 430 DDQKNETSTQT----YDSKRKNNGHVSQDSDTDLQPETTDEPLEKAYSHOLNYAECL 483
Db 384 DGTEPAGTTSNLPSSAVY--RKSCTV--DSLDIIPONNNYPRQGPFSHLUSHVSMFR 437
Qy 484 MDQRRTI----PPPTWHERSVDFFNTDAEKITQDLPVVKAYALSQASITIEGPGFTGG 538
Db 438 SGFSNSSVS1IRAPMSWTHRSAFENNIIPSSQITOPLTKSTNLGSGTSVVKGPFTGG 497
Qy 539 NLLFLIKESSNSIAKPKVTLNSAALLQRYRIRYASTNLRLFVQ----NSNNDFLV 592
Db 498 DIL-RETSPGOISTURAVNI-TAPLSQSRYRIRYASTNLQFHTS1DGRPINQCN---- 550
Qy 593 YINKTMNKDDDLTYQFDFLATNSNNMGFDXNEKYLIGAESFVSNEKITYDKEFIPVQL 652
Db 551 -FSATMSSGSNLQSGSFRTVGTIPPNFNSNGSSVFTLSAHVNSGENVYIDRIEFVPAEV 609
Db RESULT 21
A42459 parasporal crystal protein cry1Fa1 - Bacillus thuringiensis (strain aizawai)
N;Alternative names: parasporal crystal protein cry1F
C;Species: Bacillus thuringiensis
C;Date: 10-Jul-1992 #sequence_change 09-Jul-2004
C;Accession: A42459
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A;Residues: 1-1174 <CHA>
A;Cross references: UNIPROT:Q03746; GB:Me63897; PMID:91286178; PMID:2061280
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene from R;Pischhoff, D.A.; Bowdish, K.S.; Marrone, P.G.; McCormick, S.M.; Niedermeier, J.; Bacteriol., 173, 3966-3976, 1991
A;Reference number: A42459
A;Accession: A42459
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <PIS>
A;Cross-references: UNIPROT:Q93T21
A;Title: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-115 <PIS>
A;Cross-references: UNIPROT:Q93T21
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 26.4%; Score 899.5; DB 2; Length 1174;
Best Local Similarity 34.5%; Pred. No. 2.2e-19;
Matches 204; Conservative 104; Mismatches 221; Indels 63; Gaps 14;

RESULT 20
A29125 parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Accession: A29125
C;Title: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
A;Status: not compared with conceptual translation
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A;Cross-references: UNIPROT:Q93T21
C;Superfamily: parasporal crystal protein

Qy	882 VPFAGALTSPYQSLNLTIVPSDADEWKA FMAQEVLIDKIEEYAKSKALABLQGLQNMF 141	Db	107 YQIYAESPREWEADPTN -PALREBMRIQ -ENDINNSALTAIPLFAYVQVPLLSVRYQ 163
Db	49 VPGCVAFGLDFLWGFITPSD --WSSLQIQLQIERIETERNRATTGGLADSY 105	Qy	201 AANTHLLIKDAQVPEEGWYSSEDVAEPYHRQLKTQOYTDHCVNTWVNGLNGRSTY 260
Qy	142 EDYNNALNSKKTPLSLRSKRSODIRELFSQAEASHFRNSMPSFAVSKEVFLFLPTYAQA 201	Db	164 AANLHLSVLRLDVSVFQGRWGFDAATINSRNDLTRLIGHNTDAVRWNTGLERVGPD 223
Db	106 EYIEARLWEEANP --NNAQLREDVRTRFANTDDALITAINNFTLTSEIPLLSVYQA 162	Qy	261 DAWYKFNRFREMTLVLDLIVLFPFYDIRLYSKGVKTBLTRDIFTDPIFLSLNLTQEYGP 320
Qy	202 ANTHLLIKDAQVPEEGWYSSEDVAEPYHRQLKTQOYTDHCVNTWVNGLNGRSTY 261	Db	224 RDWIRYNQFRRELTLTVLDLIVLFPFYDIRLYSKGVKTBLTRDIFTDPIFLSLNLTQEYGP 278
Db	163 ANGLHLSLRDAVSVFGQMGDLIATVNHHNLINLHRTKHCLDTYNGLENURGTNTR 222	Qy	321 TF ---LSIENSIRKPHLFDYLOGIEFHTRLQPSYFKDSFNYWSGNVETRPSIGSSKT 376
Qy	262 AWKFKNRFREMTLVLDLIVLFPFYDIRLYSKGVKTBLTRDIFTDPIFLSLNLTQEYGP 321	Db	279 SFRGAQGTEGSIRSPHMDILNSITIXTDAHGEY ---YWSGHQIMASPVGFSGP 332
Db	223 QWAENQFQRDLTTLTVLDLIVLFPFYDIRLYSKGVKTBLTRDIFTDPIFLSLNLTQEYGP 321	Qy	377 ITSPFYGDK -STEPVKLSD -GOKVYKTIAINTDVAAPNGPKY ---LGVTKVDFSQY 429
Qy	3222 -FLSIENSIRKPHLFDYLOGIEFHT ---RLQPQYXFCKNSFNTWSGNVETRPSIGSSKT 376	Db	333 FTPFLYGMGNAAFPQRIVAOLQGCVYRTLSST -----LYRPPFNGINNNQQLSVL 383
Db	283 GFNRAEFGVYRPHLMDFMMSL -FVTAETRSQ ---TWGGHLVLSRNRNAGN --R 330	Qy	430 DDQKNKETSTQT -----YDSKRANGHVAQSQDSIDQLPPPTTDSPLEKAYSHQUNYAECP 483
Qy	3777 ITSPFYG-----DKSTEWPQKLSDFGQKVYRTANTDV -AAWPNGKVLGYCTK 423	Db	384 DGTEFAYGTSSNLNPSSAVY --RSGSTV --DSLDEIPPNNNVPPRGQFSHRLSHVSMR 437
Db	3331 INFPSYGVFNPNGGAIWIADEDPRP -----FYRTLSDPVEVRGCGFNPYVHLGRG 380	Qy	484 MQDRRTGI -----PFETPTWHSYDFDENTIDAEEKITQPVVKAYAASSGASIIEGPQFTGC 538
Qy	4244 VDFRQYQDDKNETSTQTYDSKRANGHVAQSQDSIDQLPPPTTDSPLEKAYSHQUNYAECP - 482	Db	438 SGFSNSVSSVIRAPMFWSIHSRANSNNIIPSSQITQIPLKTSKTNLGSITVKGPFGTG 497
Db	3881 VAFQQ -----TGTMNHTTFRNSGTI --DSLDEIPPDNSGAPWNDYSHVLNHVTFTV 430	Qy	539 NLLPLKKESSNSIAKFKTYTNSAALLQYRVRVRYAATSNLURLFVQ ---NSNNDFLVI 592
Qy	4833 ---LMQDDRGTIPFPTWTHRSDFFNTIDAEEKITQPVVKAYAASSGASIIIEGPQFTGC 538	Db	498 RLTSPGQISITLRYNI -TAPLSQYRVRVRYAATSNLQFHTSISHPRINQCN ----- 550
Db	4311 WPGELISGSSESWRAPMFWSWHSRATPTNTIDPERITQIPPKVAKHTLQSSTGTTVWRGPQFTGC 490	Qy	593 YINKTMNKDDDLIAYQTFDLATNSNMGSFQDNLIELIGAESFVSNEKTYIDKEFIPVQL 652
Qy	5399 NLJFLIKESSNSIAKFKVTLNSAAILQYRVRVRYAATSNLRLFVQNSNNDFLYIYNTM 598	Db	551 -FSATMSSGSNLQSGSFRLHGLFTTPFNSNGSSVFTLSAHVNSGNEVYIDRIEFVPAEV 609
Db	491 DI --LRRTGPPFAYTIVNGQLPQRYARIRYASTTNLRIVTVAZERIFAGQFNKTM 548	RESULT 23	
Qy	599 NKDDDLTYQFDLATNSNMGSFQDNLIELIGAESFVSNEKTYIDKEFIPV 650	A4:1052	parasporal crystal protein cryAel - Bacillus thuringiensis (strain alest1)
Db	549 DTGBPLTRFQSFTATINTAFTFPMQSSTTGVADTFSSGNEVYIDRFELIPV 600	C:Species: Bacillus thuringiensis	
		C:Date: 03-Apr-1992 #Sequence_revision 03-Apr-1992 #text_change 09-Jul-2004	
		C:Accession: A41052; MUID:92011442; PMID:1655719	
		R;Lee, C.S.; Aronson, A.I.	
		J. Bacteriol. 173, 665-6638, 1991	
		A:Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp R;Lee, C.S.; Aronson, A.I.	
		A:Reference number: A41052; MUID:92011442; PMID:1655719	
		A:Accession: A41052	
		A:Status: preliminary	
		A:Molecule type: DNA	
		A:Residues: 1-1181 <LEB>	
		A:Cross-references: UNIPROT:Q03748; GB: M65252; NID: G142874; PID: G142875	
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		C:Keywords: delta-endotoxin	
		Query Match 26.1%; Score 888; DB 2; Length 1181;	
		Best Local Similarity 34.6%; Pred. No. 1..1e-48;	
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Qy	139838 parasporal crystal protein - Bacillus thuringiensis	Qy	82 VPPAGALTSPYQSLNLTW ---PSADDPWKAFAQVEVLIDKIEEYAKSKALELQL 137
C:Species: Bacillus thuringiensis	C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004	Db	51 VPGAG ---FVGLGLDLIWGFVGPSSQ ---WDAFLVQIEQOLISQRIEFARNQAISSLG 103
C:Accession: I39838	C:Accession: I39838	Qy	138 QNNFEDYNNALNEWKTKPLSLRSRKSQRDIRELFSQABSHFRNSMSPFAVSKFELVFLPT 197
R;Hefford, M.A.; Brouseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.	J. Biotechnol. 6, 307-322, 1987	Db	104 SNLYQIYAAEFAFEMEADPTN -PALREBMRIQ -FNDMNSALITAIPPLFTVQNYQVPLLSV 160
A:Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki	A:Reference number: I39838	Qy	198 YAORANTHLLIKDAQVFEGLWVQGEEWYSSVEDAEFYTHRQLKTQOYTDCVNTWVNGLNGR 257
A:Accession: I39838	A:Accession: I39838	Db	161 YQVANLNLHSVLDVSVQRMGLDVAUTNSRNDRFLIGHTDIAWRWNTGLERVG 220
A:Status: preliminary; translated from GB/EMBL/DDBJ	A:Status: preliminary; translated from GB/EMBL/DDBJ	Qy	258 STYDWWVKNPFRREMTLTVLDLIVLFPFYDIRLYSKGVKTELTRDIFTDPFLSNTLQ 317
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C:Superfamily: parasporal crystal protein	C:Superfamily: parasporal crystal protein	Qy	
Qy	31 DNPNSTLEELNQYKEFLRMTEDSSTEVLNISTVDAVGTCISVWG ---QILGVVGVYP 84		
Db	3 NNPNIN-ECIY ---NCIISNPVEVUGGERIE ---TGTYPIDISLSTOFLLSEFVG 53		
Qy	85 AGALTSFYQSLNLTW ---PSADDPWKAFAQVEVLIDKIEEYAKSKALELQL 140		
Db	54 AG ---FVGLGLDLIWGFVGPSSQ ---WDAFLVQIEQOLISQRIEFARNQAISSLG 106		
Qy	141 FEDVNLNSKKTPLSLRSKRSQRDIRELFSQAEASHFRNSMPSFAVSKEVFLFLPTYAQ 200		

318	YGPFLS---IENISRKPFLDYLOGIEFHTRLQPGYFGKDFNTYNSGNYVETRPSIGS	373	Qy	411 AWPNGKTYL-GVTKVDESQYDDQKNETSTQYDSKRNGHYSQAQS DQLEPBTTEPEOPLE	469
276	FDGSGERGSQRIBOSIRSPHMLDILNSITIYTDAHGGY-	329	Db	375 PMPAPPFNLRGVGEVES-----TPNLS-----	422
374	SKTTSPEFYGDK-STEPVYKLSFD-GOKYVRTIANTDVAAWPNCKVYLGVTKVDFSQYDD	431	Qy	470 KAYSHQOLNYAECFLMQLQDRGTI-----PFPFWTHRSDFENTIDAEEKITOLPVVKAYALS	524
330	GPEFTPLYCTGMGNAPQORIVAQDQGQYRTLST---FYRNPFLGINNQRLSVLDG	385	Db	423 EGTSRSGTFLPLTGPFSMTHRSATDRNITYPDINQIPVKANLT	479
432	QK--NETSTQTYDSKRNGHVSQAQS DSIQDLPPTTDEPLEKAYSHQNLAECCFLMQDR	488	Qy	525 SGASIIEGPQFTGCGNLFLKESSNSIAKEFKVTLN-SALLQYRVRVRYASTNLRLRFV-	582
386	TEFAFQSSSLPSPAVYRKSTV---DSLDPQDNVNPFRQSFHRSVLHSMSRSGFSN	442	Db	480 SGTSVVRGFGTQGDIRTNVNGSVLS--MSLNFNSTLQYRVRVRYAASTMWSVT	536
489	GTI----PFPFWTHRSDFNTIDEAKITOLPVKAYVALSSGASIIEGPQFTGCGNLFL	543	Qy	583 ---QNSNNDELVJYIYKUMNKDDLTQTFDIAATTNNMGFSGDKNEELIGAESFSN-	637
443	SSVS1IRAPMFSWIRSAETNNIIPSPQTQIPLKSTNLSGTSVVKRGFGTQGDIL-R	501	Db	537 VGGSTTGNGCF-----PSMSANGALTSCSFRFAEPVGISASGSQ-----GASISISNN	586
544	KESNSIAKPKVTLNSAALLLORYRVRVYRSTTNLRLFVQ-----NSNNDELVYIYKT	597	Qy	638 ---EKYIYDVKIEKFIPV	602
502	RTPSPGQISTLRVN-TAPLSORYRVRVYRSTTNLOFHTS1DGRPINQGN-----FSAT	554	Db	587 VGRQMFHLDRIEFLPV	602
RESULT 25					
	JT0241				
	parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)				
	N;Alternate names: 135K insecticidal protein				
	C;Species: Bacillus thuringiensis				
	C;Date: 31-Mar-1992 #sequence_change 09-Jul-2004				
	C;Accession: JT0241				
	C;Sequence_revision 31-Mar-1992				
	A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal				
	A;Reference number: JT0241				
	A;Accession: JT0241				
	A;Molecule type: DNA				
	A;Residues: 1-176 <SHI>				
	A;Cross-references: UNIPROT:PO2965				
	A;Comment: The 135K protein produces similar 130K and 135K insecticidid activity against Plutella xylostella				
	C;Superfamily: parasporal crystal protein				
	C;Keywords: delta-endotoxin				
	Query Match	25.7%	Score 876; DB 2; Length 1176;		
	Best Local Similarity	32.9%	Pred. No. 6.2e-48;		
	Matches 215; Conservative 120; Mismatches 240; Indels 78; Gaps 22;				
	Qy	31 DNPNSTLRELNYKEFLRMTEDSSTEVIDNSTVYKSKALABLOGLN	84		
	Db	3 NNPNIN-ECIPY---NCLSNPEVEVLGGERIE---TGYPIDISLSLTOFLSBFVPG	53		
	Qy	85 AGALTSEYQSEFLNTIW----PSDADPKAQMAGQEVLIDKKBLYAKSKALABLOGLN	140		
	Db	54 AG---FVGLDLIWWGFGPSQ--WDAFLVQIEQLINQRIEEFARNQASISLGSLNL	106		
	Qy	141 AGDVNALNSWKTPLSLRSKRSODTRLEFLSQAESHRFNRNSMPSFAVSKFEVLFPLTVYAQ	200		
	Db	107 YQIYAESFREWEADPTN-PALREMRRIQ-FNDKNSALTAIPLAVONYQVLLSIVYQ	163		
	Qy	201 AANTHLLIKDAQVFLGEEMGSSVEDAEEFHQLKLQTQYTDHCYWNVNGLNGLRGSTY	260		
	Db	164 AANLHLSSLVDFQRMGFDATINSRNLTRLIGHYDFAWRWTNLGLERWGPD	223		
	Qy	261 DAWYKFNRFREMTLVLDLIVLFYDRLYKSKVKELTTRDIFPLSILNLQYEGP	320		
	Db	224 RDWYIYNQFRELTITLVLDIVALEFSNYDSRYPTRTVSOLTRETYNTPV-----LENFDG	278		
	Qy	321 TFLS---IENSIRKPHFLPYLOGBFHTRLQPGYFGKOSFNTNSGNYVETRPSIGSSKT	376		
	Db	279 SFRGAQRIEINIRPHMLINSLTIVYDVRHRC-----ENYQGHQ:TASPVSFGSP	332		
	Qy	300 LTRDIFTPIFSLN-TLQEYG--PTFLSIE NSIRKPHFLPYLOGBFHTRLQPGYFGKD	355		
	Db	262 LTREYDPLTPIFNQQLQSVADLPTFNMEAIRPHFLDNNTLIFTI-----DMFSVG	317		
	Qy	357 ITSPFGDK-STEPVYKLSFPGQKYRTIAN-----TDVAWPNGKVLGYTKVDFSQYD	430		
	Db	333 FAFLPGNAGNAAPPLVSLTGLGFRFTLSNPTFRPLQQ	392		
	318 RNFYWGCHRVTSN-RIGGG-NITSPYGREENQEPPSFTFNG-PVFTLNSPTFRPLQQ	374			

Qy	431. DQNETSTOTYDSKRNNGHIVSAQDSIDQLUPEPTDEPLKAYSHQLNAYAECFCIMQDRGGT 490	Db	444 VYTLPAPTSWQRSAEFTNIISSQITQIPLXSTNLGSGTSVKGPFETGGDIL-RRT 502
Db	393 LTNLPST---IYQRGTV--DSLDPVTPQDNISVPPRAGFSHRLSHVT--MLSQAGA 443	Qy	546 SNSIAKEFKVTLNSAALLORYRYRIRYASTTNRLFVQ----NSNNDFLVYINKTMN 599
Qy	491. I----PFPFWHRSVDFFNTIDAEEKITOLPVLVKAIALSGASITIEGPGFTGGNLLFLKE 545	Db	503 SPGQISTLRVNI-TAPLSQYRIRYRIRYASTTNRLFVQ----FSATMS 555
Db	444 VYTLPAPTSWQRSAEFTNIISSQITQIPLXSTNLGSGTSVKGPFETGGDIL-RRT 502	Qy	600 KDDDLTYQFDLATTNSNMGSFDDKNEELIGAESPSVSNKIVYDKEFIPVOL 652
Qy	546 SNSIAKEFKVTLNSAALLORYRYRIRYASTTNRLFVQ----NSNNDFLVYINKTMN 599	Db	556 SGSNLQSGSFRTVGFTTPNFNSGSSVFTLSAHYFNSGNBVIIDRIEFVPAEV 608
Db	503 SPGQISTLRVNI-TAPLSQYRIRYASTTNRLFVQ----FSATMS 555	RESULT 27	
Qy	600 KDDDLTYQFDLATTNSNMGSFDDKNEELIGAESPSVSNKIVYDKEFIPVOL 652	JC2219	parasporal crystal protein crylha - <i>Bacillus thuringiensis</i>
Db	556 SGSNLQSGSFRTVGFTTPNFNSGSSVFTLSAHYFNSGNBVIIDRIEFVPAEV 608	C;Species:	<i>Bacillus thuringiensis</i>
A22798	parasporal crystal protein - <i>Bacillus thuringiensis</i>	C;Accession:	JC2219
C;Species:	<i>Bacillus thuringiensis</i>	C;Accession:	28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession:	A22798	C;Accession:	23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
R;Shibano, Y. : Yamagata, A. : Nakamura, N. : Iizuka, T. : Sugisaki, H. : Takanami, M.	A;Title:	A;Reference number: JC2219; MUID:94289859; PMID:7764972	
Gene 34, 243-251, 1985	A;Residue:	A;Molecule type: DNA	
A;Title: Nucleotide sequence coding for the insecticidal fragment of the <i>Bacillus thuringiensis</i> A;Reference number: A22798 ; MUID:2989108	A;Residues:	A;Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:9506190; PIDN:BAA04468.1; PID:95357	
A;Accession: A22798	A;Molecule type: DNA	C;Keywords: cryIA(a)	
A;Accession: A22798	A;Molecule type: DNA	C;Superfamily: parasporal crystal protein	
A;Residues: 1-934 <SHL>	A;Residues: 1-934 <SHL>	C;Keywords: delta-endotoxin	
Query Match 26	Score 874; DB 2; Length 934;	Query Match 26	Score 870; DB 2; Length 1176;
Best Local Similarity 32.9%; Pred. No. 5.0e-48;	Best Local Similarity 32.8%; Pred. No. 1.5e-47;	Best Local Similarity 32.8%; Pred. No. 1.5e-47;	Length 1176;
Matches 215; Conservative 120; Mismatches 241; Indels 78; Gaps 22;	Matches 214; Conservative 120; Mismatches 241; Indels 78; Gaps 22;	Matches 214; Conservative 120; Mismatches 241; Indels 78; Gaps 22;	
Qy	31 DNPNSTLRELNYKEFLRMTEDSSTEVLNDNSTVDAVGTGTSVYVG-----QIGGVGVPF 84	Qy	31 DNPNSTLRELNYKEFLRMTEDSSTEVLNDNSTVDAVGTGTSVYVG-----QIGGVGVPF 84
Db	3 NNPNN-N-ECIPY---NCISNPNEVEVUGGERIE---TCYTPIDISLSTOFILSEFVPG 53	Db	3 NNPNN-N-ECIPY---NCISNPNEVEVUGGERIE---TCYTPIDISLSTOFILSEFVPG 53
Qy	85 AGALTSFYQSFLNTIW---PSDADPKWAKFMAQVEVLIDKKBIEYAKSKALAELQGLQN 140	Qy	85 AGALTSFYQSFLNTIW---PSDADPKWAKFMAQVEVLIDKKBIEYAKSKALAELQGLQN 140
Db	54 AG---FVGLVLDIWIQFGPSQ--WDAFLVQEQLINQRIEEFARNOAISRLLEGSQLN 106	Db	54 AG---FVGLVLDIWIQFGPSQ--WDAFLVQEQLINQRIEEFARNOAISRLLEGSQLN 106
Qy	141 FEDYVNALNSWKTKPLSLRSKRSODRTRFLSQAESHRNSMPSFAYSKEVIFLPTYAQ 200	Qy	141 FEDYVNALNSWKTKPLSLRSKRSODRTRFLSQAESHRNSMPSFAYSKEVIFLPTYAQ 200
Db	164 AANLHSVLRDVSFQRWGFDATINSRYNDLTRLIGNYTDYAVRWNTGLERWGPDS 223	Db	164 AANLHSVLRDVSFQRWGFDATINSRYNDLTRLIGNYTDYAVRWNTGLERWGPDS 223
Qy	107 YQIYAESPREWEADPTN-PALREEMRIO--FNDMNSAIIITAIPLLAVQNYQVPLLSVYQ 163	Qy	107 YQIYAESPREWEADPTN-PALREEMRIO--FNDMNSAIIITAIPLLAVQNYQVPLLSVYQ 163
Db	201 AANTHLLIKDAQYFGEWGYSSDABFYHROQLKTQOYTDHCVNNTVNGLNRGSTY 260	Db	201 AANTHLLIKDAQYFGEWGYSSDABFYHROQLKTQOYTDHCVNNTVNGLNRGSTY 260
Qy	164 AANLHSVLRDVSFQRWGFDATINSRYNDLTRLIGNYTDYAVRWNTGLERWGPDS 223	Qy	201 AANTHLLIKDAQYFGEWGYSSDABFYHROQLKTQOYTDHCVNNTVNGLNRGSTY 260
Db	261 DAVKFNFRREMTLTVDLIVLQPFYDIRLYSKVKTBLDRIFTDFISNLTLQBYGP 320	Db	201 AANTHLLIKDAQYFGEWGYSSDABFYHROQLKTQOYTDHCVNNTVNGLNRGSTY 260
Qy	224 RDWTRYNQFRREMTLTVDLIVLQPFYDIRLYSKVKTBLDRIFTDFISNLTLQBYGP 320	Qy	164 AANLHSVLRDVSFQRWGFDATINSRYNDLTRLIGNYTDYAVRWNTGLERWGPDS 223
Db	321 TFLS----IENSIRKPHLFYLOGIEFHTRLQDGFYFKDSFNPWNSGNVETRPSIGSSKT 376	Db	224 RDWTRYNQFRREMTLTVDLIVLQPFYDIRLYSKVKTBLDRIFTDFISNLTLQBYGP 320
Qy	321 TFLS----IENSIRKPHLFYLOGIEFHTRLQDGFYFKDSFNPWNSGNVETRPSIGSSKT 376	Qy	224 RDWTRYNQFRREMTLTVDLIVLQPFYDIRLYSKVKTBLDRIFTDFISNLTLQBYGP 320
Db	279 SFGMAQDIEQNIQPHMDILNRITYDVHRC----FNYWSGHQITASPVGFGFQPE 332	Db	321 TFLS----IENSIRKPHLFYLOGIEFHTRLQDGFYFKDSFNPWNSGNVETRPSIGSSKT 376
Qy	377 ITSPFYGDK-STPVQKLISFDGOKVYRTIAN---TDVAAMPNGKTYLGTVKUDFQSD 430	Qy	321 TFLS----IENSIRKPHLFYLOGIEFHTRLQDGFYFKDSFNPWNSGNVETRPSIGSSKT 376
Db	333 FAPPFGNAGNAAPPVLYSLTGIGIERTLSSPLYRRLGSGENNOELFVLDGTEFFFAS 392	Db	377 ITSPFYGDK-STPVQKLISFDGOKVYRTIAN---TDVAAMPNGKTYLGTVKUDFQSD 430
Qy	431 DQNETSTOTYDSKRNNGHIVSAQDSIDQLUPEPTDEPLKAYSHQLNAYAECFCUMQDRGRT 490	Qy	333 FAPPFGNAGNAAPPVLYSLTGIGIERTLSSPLYRRLGSGENNOELFVLDGTEFFFAS 392
Db	393 LTNLPST---IYQRGTV--DSLDPVTPQDNISVPPRAGFSHRLSHVT--MLSQAGA 443	Qy	377 ITSPFYGDK-STPVQKLISFDGOKVYRTIAN---TDVAAMPNGKTYLGTVKUDFQSD 430
Qy	491 I----PFPFWHRSVDFFNTIDAEEKITOLPVLVKAIALSGASITIEGPGFTGGNLLFLKE 545	Db	393 LTNLPST---IYQRGTV--DSLDPVTPQDNISVPPRAGFSHRLSHVT--MLSQAGA 443
		Qy	491 I----PFPFWHRSVDFFNTIDAEEKITOLPVLVKAIALSGASITIEGPGFTGGNLLFLKE 545

Db	503	SPGQISTLRRVNI-TAPLSQRQYRVRIRYASTTNLQFHTSICGRPINQGN-----FSATMS	555	Db	549	EIGESELSRTSRFTSYTNFSNPFSSFRANPDIRIABELPIRGGBLYIDKIELI	598
Qy	600	KDDDLTYQTDFIATINSMNGSGDKNELIIGAESPTSNNEKLYIDKIEFIPVQL	652	RESULT 29			
Db	556	SGSNLQSGSFRTVGFITPENFSNGSSVFTLSAHVENSNEVYDRIEFVFAEV	608	A37829	Bacillus thuringiensis		
				C;Species: Bacillus thuringiensis	parasporal crystal protein cry1Ba1 - Bacillus thuringiensis		
				C;Date: 14-Jun-1991 #sequence revision 03-May-1994 #text_change 09-Jul-2004			
				C;Accession: A37829; S33762; S14438			
				R;Visser, B.; Munsterman, E.; Stoker, A.; Dirks, W.G.			
				C;Title: J. Bacteriol. 172, 6783-6788, 1990			
				A;Title: A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-specific crystal protein			
				A;Reference number: A37829; MUID:91072224; PMID:2254254			
				A;Accession: A37829			
				A;Molecule type: DNA			
				A;Residues: 1-1171 <VI2>			
				A;Cross-references: UNIPROT:006894; EMBL:X53985			
				A;Translation is incomplete			
				C;Superfamily: parasporal crystal protein			
				C;Keywords: delta-endotoxin			
				Query Match 25.5%; Score 869.5; DB 2; Length 1171;			
				Best Local Similarity 33.7%; Pred. No. 1..6-47;			
				Matches 219; Conservative 117; Mismatches 241; Indels 73; Gaps 21;			
				Query 19 ELQTMHNQ--YPLADNPNSTLEELNKYKEFLRMTEDSSTEVLNDNSTVKDAVGTG1SVVGQ	75		
				2 EIVNNQNCVPNCNLNPEN-----			
				Db 76 ILGVGVPPAGALTSFYQSPLNTIWPSPDAPWKAQMVEFLDKEEYAKSKAALELQ	135		
				Db 43 RLLASATPIGGILSLFDI1WGSIGPSQ--WDLFLEQIELLIDQIEEFARNQAIISRL	99		
				Qy 136 GLQNNFEDYNALNEWKKTPSLRSKRSQSPREIFSOAESHFNNSMPAVSKPEVFL	195		
				Db 100 GISSLQGIYTEAFREWEEADPTNPALK--BEMRTOFDMDNSILVTAPIPLESQVNTQVPFL	156		
				Qy 196 PTYAQAANTHILLIKDQAVQFELTQDLYTQYTDHCVNWYNGLN--	253		
				Db 157 SVYVQANLHLISVLRVSVFGQANGQFDIATINSRNDLPLRIPYTDYAVRWYNGLDRL	216		
				Qy 254 ---GLRGSTYDAWTKFNFRFREMTLVTDLIVLPFYDILYSKGKTELTRDIFTDP	309		
				Db 217 PRTGGERN---WARENQFRELTSVLDLISFRYDPLTSPQLTREVYTDPV	271		
				Qy 310 FSLNTLQEYQGTFLSLENS-TRKPHFDYDQGIEBPHTRLOGYFGGDSFNYWSGNVYETR	368		
				Db 272 INI-TIYRGPSFENTENSAARSPLMDFLNLNTDTDLIRG---VYWWAGHRV-TS	323		
				Qy 369 PSIGSSKTITSPTFYG-DKSTEP---VOKLSEFDGOKW-YRTIANTDVAAPNGKVYLGVTK	423		
				Db 324 HFTGSSQVTRIPQYGTANABPRITAFTPSLNPFPFRSERNTPTPLGINV	383		
				Qy 424 VDFSDQDDQNETSTQTYDSKRNNGHVSAQDSIDOLQPETDEPLKAYSHOLNYAEC--	481		
				Db 384 VQGVGFQPNN--AEVLY--RSRGTV--DSUNELPIDGENSLV-GYSHRLSHVTLTR	493		
				Qy 542 FLKESSNSIAKF---KVTLNEAALLORYVRTRIYASTTNLRLFVQNSNNDEFLVYINKTM	598		
				Db 494 ---RNNTGEVFLQVNINS-PITQRTLRPFYASSRDIARITAIGQIRDMTLEKTM	548		
				Qy 599 NKDDDTYOTFELATTNSNMGFSGDKNELIIGAESFVSNEKLYIDKIEFI	648		
				Db 549 EIGESELSRTSRFTSYTNFSNPFSSFRANPDIRIABELPIRGGBLYIDKIELI	598		
				C;Accession: A49785	parasporal crystal protein cry1A(c) - Bacillus thuringiensis subsp. kenyaе (strain HD588-		
				Qy 599 NKDDDTYOTFELATTNSNMGFSGDKNELIIGAESFVSNEKLYIDKIEFI	648		

RESULT 30
A49785

C;Species: Bacillus thuringiensis subsp. kenyaee
 C;Accession: A49785
 R; Von Tersch, M.A.; Robbins, H.L.; Jany, C.S.; Johnson, T.B.
 Appl. Environ. Microbiol. 57, 349-358, 1991
 A;Title: Insecticidal toxins from *Bacillus thuringiensis* subsp. kenyaee: gene cloning and
 A;Reference number: A49785; PMID:91197102;
 A;Accession: A49785
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-1177 <VON>
 A;Cross-references: UNIPROT:Q45735; GB:M35524; NID:gi42739; PIDN:AAA22338.1; PID:gi42740
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 25.5%: Score 867.5; DB 2; Length 1177;
 Best Local Similarity 33.7%; Pred. No. 2.2e-47;
 Matches 220; Conservative 110; Mismatches 242; Indels 81; Gaps 24;

Qy 31 DNPISTLELNKYKEFLRMTEDSSTEVLNDNSTKDAVGTTISVVG-----QIIGVVGVYPF 84
 Db 3 NNPNIN-ECIPIY----NCISNPVEVLLGGERIE---TCYTPIDISLSITQELISEFVFG 53

Qy 85 AGALTSFYQSFLNTW---PSDADPKAFMAQVEVLDDKKTIEYAKSKALARLQLGQN 140
 Db 54 AG---FVGLVDIWIWGIGPSQ--WDAFLVQEQLINQRIEEFARNQAIISLEGLSNL 106

Qy 141 FEDYNALNSWKTKPLSLRSKRSQRDRILFLSQAESHPNSMSFAVSKFEVLFLPITYAQ 200
 Db 107 YQIAESFPEWEADPTN-PALREEMRIO--ENDMNSALTAIPLAVVQYQVPLLSVYQ 163

Qy 201 AANTHLLIKDAQVFGEEGYSSSEVEDAEPYTHRQLKLTOQYTDICVANWNNGLRLGSTY 260
 Db 164 AANLHSVLRDVSVFGQRGFDAATINSRYNDLTTRIGNYTDIAVRWTNTGLERVWGPDS 223

Qy 261 DAWYKFNRFRREMTLTVLIVLPFFYDYLRLSKGVKTFLTRDIFTDPTFSINTLQTYGP 320
 Db 279 SFRSAQGGRSIRSRSRPHMDLNSITVDAHGGY----YWSGHOMASVGFSCPE 332

Qy 377 ITSPYGDK-STEPVQKL-SFD-GOKVYRTIANTDVAAMPNGKVLYGVTKVDFSDQYDQKN 434
 Db 333 FTFLYGMNAAPQQRIVTAAQLGQGVYRTLSST---FYRRPNIGINNQQLSVLDGTET 388

Qy 435 ETSTQT-----YDSKRKNRGHVAQDSDTQLPPPTDEPLEKAYSHQUNYAECFLMQRDR 488
 Db 389 AYGTSSNLSAVY--RKSGTV--DSDELIPONNNVPQPROFSHRLSHVSMF---RS 438

Qy 489 GT-----IPFTTWTHRSVDFNTIDEKTLQPLPVKAYAASSGASIEPGFTGQN 540
 Db 429 GSSSSVSLRAPMFSWIRSAEPPNNTIASDTSITQPAVGNFLFNG-SVISGEGFTGDL 497

Qy 541 LFLKESSNSIAK--FKVTLNSAALLQYRVRVRYASTNLFLVQNSNNDLFLVITNK 597
 Db 498 VRLNSSGNNNTQNRQXYIEVTHFPSTSTRYVRVRYASSTPIHLNVNGNNSISFSNTVPA 557

Qy 598 MNKDDLIYQTFDLATINSMGFSGDKNBLIIGAESFVNEKUYDKIEFIPV 650
 Db 558 ATSLDNL-QSSDFGYFESSANAFTSSLGN-IVGVRNFGTAGVYIDRFEFIPV 607

RESULT 31
 USBXKH
 Parasporal crystal protein cry1Ac1 [validated] - *Bacillus thuringiensis* subsp. kurstaki
 C;Species: *Bacillus thuringiensis* subsp. kurstaki
 C;Date: 18-Apr-1984 #Sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C;Accession: A23862; A03489
 R;Adang, M.J.; Stever, M.J.; Rocheleau, T.A.; Leighton, J.; Barker, R.F.; Thompson, D.V.
 Gen 36, 289-300, 1985
 A;Title: Characterized full-length and truncated plasmid clones of the crystal protein d

A;Reference number: A91526; MUID:86083171; PMID:3000881
 A;Accession: A23952
 A;Molecule type: DNA
 A;Residues: 1-1178 <ADA>
 A;Cross-references: UNIPROT:P05068; GB:MI1068; NID:gi42721; PIDN:AAA22331.1; PID:gi42722
 A;Experimental source: strain HD-73
 A;Note: The authors translated the codon ATT for residue 11 as Leu
 R;Wong, H.C.; Schnepf, H.E.; Whiteley, H.R.
 J. Biol. Chem. 258, 1960-1967, 1983
 A;Title: Transcriptional and translational start sites for the *Bacillus thuringiensis* cr
 A;Accession: A03489
 A;Reference number: A92410; MUID:83105004; PMID:6296116
 A;Molecule type: DNA
 A;Residues: 1-76, 'P', '78-147', 'L', '149-247', 'S', '249-282, 'M', '284-285, 'R', '287-288, 'QN', '291-292
 A;Experimental source: strain HD-1
 C;Comment: This protein is present in crystalline form as a component of the spore coat.
 C;Superramia: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 25.5%: Score 867; DB 1; Length 1178;
 Best Local Similarity 33.4%; Pred. No. 2.3e-47;
 Matches 219; Conservative 112; Mismatches 240; Indels 84; Gaps 24;

Qy 31 DNPNSTLRELNYKEFLRMTEDSSTEVLNDNSTKDAVGTTISVVG-----QIIGVVGVYPF 84
 Db 3 NNPNIN-ECIPIY----NCISNPVEVLLGGERIE---TCYTPIDISLSITQELISEFVFG 53

Qy 85 AGALTSEYQSFLNTW---PSDADPKAFMAQVEVLDDKKTIEYAKSKALARLQLGQN 140
 Db 54 AG---FVGLVDIWIWGIGPSQ--WDAFLVQEQLINQRIEEFARNQAIISLEGLSNL 106

Qy 141 FEDYNALNSWKTKPLSLRSKRSQRDRILFLSQAESHPNSMSFAVSKFEVLFLPITYAQ 200
 Db 107 YQIAESFPEWEADPTN-PALREEMRIO--ENDMNSALTAIPLAVVQYQVPLLSVYQ 163

Qy 201 AANTHLLIKDAQVFGEEGYSSSEVEDAEPYTHRQLKLTOQYTDICVANWNNGLRLGSTY 260
 Db 164 AANLHSVLRDVSVFGQRGFDAATINSRYNDLTTRIGNYTDIAVRWTNTGLERVWGPDS 223

Qy 261 DAWYKFNRFRREMTLTVLIVLPFFYDYLRLSKGVKTFLTRDIFTDPTFSINTLQTYGP 320
 Db 224 RDWTRYNQFRRELTFLVLDIVLPFFYDYLRLSKGVKTFLTRDIFTDPTFSINTLQTYGP 328

Qy 321 TF---LSIENSTRKPHLFDYLOGIEPHTRLQDGPYFKDSFENYSGNVETRPSIGSSRT 376
 Db 279 SFRGSAQGIERSTRSPHLMDLNSITVDAHGGY----YWSGHOMASVGFSCPE 332

Qy 377 ITSPYGDK-STEPVQKL-SFD-GOKVYRTIANTDVAAMPNGKVLYGVTKVDFSDQYDQKN 434
 Db 333 FTFLYGMNAAPQQRIVTAAQLGQGVYRTLSST---FYRRPNIGINNQQLSVLDGTET 388

Qy 435 ETSTQT-----YDSKRKNRGHVAQDSDTQLPPPTDEPLEKAYSHQUNYAECFLMQRDR 488
 Db 389 AYGTSSNLSAVY--RKSGTV--DSDELIPONNNVPQPROFSHRLSHVSMF---RS 438

Qy 489 GT-----IPFTTWTHRSVDFNTIDEKTLQPLPVKAYAASSGASIEPGFTGQN 540
 Db 429 GSSSSVSLRAPMFSWIRSAEPPNNTIASDTSITQPAVGNFLFNG-SVISGEGFTGDL 497

Qy 541 LFLKESSNSIAK--FKVTLNSAALLQYRVRVRYASTNLFLVQNSNNDLFLVITNK 597
 Db 498 VRLNSSGNNNTQNRQXYIEVTHFPSTSTRYVRVRYASSTPIHLNVNGNNSISFSNTVPA 557

Qy 598 MNKDDLIYQTFDLATINSMGFSGDKNBLIIGAESFVNEKUYDKIEFIPV 650
 Db 558 ATSLDNL-QSSDFGYFESSANAFTSSLGN-IVGVRNFGTAGVYIDRFEFIPV 607

RESULT 32
 S32645
 Parasporal crystal protein cry1Gal - *Bacillus thuringiensis*
 C;Species: *Bacillus thuringiensis* subsp. kurstaki
 C;Date: 18-Apr-1984 #Sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C;Accession: A23862; A03489
 R;Adang, M.J.; Stever, M.J.; Rocheleau, T.A.; Leighton, J.; Barker, R.F.; Thompson, D.V.
 Gen 36, 289-300, 1985
 A;Title: Characterized full-length and truncated plasmid clones of the crystal protein d

Qy 596 KTMNKDDLIYQTFDLATINSMGFSGDKNBLIIGAESFVNEKUYDKIEFIPV 650
 Db 557 ATSLDNL-QSSDFGYFESSANAFTSSLGN-IVGVRNFGTAGVYIDRFEFIPV 608

Best Local Similarity 32.8%; Pred. No. 2.7e-47; Matches 214; Conservative 119; Mismatches 242; Indels 78; Gaps 22;		Db 3 NYPIN-ECIPY---NCLSNPEVEVLLGERIE---TGYTPIDISLSLTOFLLSEFVG 53	
Qy 31 DNPNSTLEELNYKEFLRMTEDSSTEVLNDSTKDAVGIGISVG-----OrIgvavpp 84	Qy 85 AGATTSFVQSFINTIW---PSDADPKAFMAQVEVLIDKKKEEYAKSKALAEQGLQNN 140	Db 54 AG---FVGLVDIINGFGPSQ---WDAFLVQIEQLINQRTEFPARNQAISSLLEGSLNL 106	
Qy 85 AGALTTSFOSFLSRLSRSKRSODRLEFLSQDESHFRNSMPSFAYSKEVFLPVAQ 53	Qy 141 FEDYVNALNSWKTKPLSLRSRSKRSODRLEFLSQDESHFRNSMPSFAYSKEVFLPVAQ 53	Db 107 YQIYAESPREWEADPTN-PALREEMRQ-Q---FDMDNSALTAIPLAIVQYQPLSVYQ 163	
Db 54 AG---FVGLVDIINGFGPSQ---WDAFLVQIEQLINQRTEFPARNQAISSLLEGSLNL 106	Qy 141 FEDYVNALNSWKTKPLSLRSRSKRSODRLEFLSQDESHFRNSMPSFAYSKEVFLPVAQ 200	Db 107 YQIYAESPREWEADPTN-PALREEMRQ-Q---FDMDNSALTAIPLAIVQYQPLSVYQ 163	
Qy 141 FEDYVNALNSWKTKPLSLRSRSKRSODRLEFLSQDESHFRNSMPSFAYSKEVFLPVAQ 200	Qy 201 AANTHLLIKDAQVEGKYSSEDEVAFHQQLKLQQTYCUDENAVNGLNGLRSTY 260	Db 164 AANLHLSSVLRDVSVFGRGDFDAATINSRYNLDLRLIGNTYDQAVRNNTGLERVWGPDS 223	
Db 107 YQIYAESPREWEADPTN-PALREEMRQ-Q---FDMDNSALTAIPLAIVQYQPLSVYQ 163	Qy 201 AANTHLLIKDAQVEGKYSSEDEVAFHQQLKLQQTYCUDENAVNGLNGLRSTY 260	Qy 261 DAWKVNFRFRENTLTVDLIVLPFFDIRLYSKGVKTELTRDIFTDPIFSINTLQEVGP 320	
Qy 201 AANTHLLIKDAQVEGKYSSEDEVAFHQQLKLQQTYCUDENAVNGLNGLRSTY 260	Qy 261 DAWKVNFRFRENTLTVDLIVLPFFDIRLYSKGVKTELTRDIFTDPIFSINTLQEVGP 320	Db 224 RDWTRYNQFRRSLTITLTDIVALFPNDSRRPRTYSQLTRBYITNPV---LENFDG 278	
Db 164 AANLHLSSVLRDVSVFGRGDFDAATINSRYNLDLRLIGNTYDQAVRNNTGLERVWGPDS 223	Qy 261 DAWKVNFRFRENTLTVDLIVLPFFDIRLYSKGVKTELTRDIFTDPIFSINTLQEVGP 320	Qy 321 TF---LSIENSTRKPHLFDVLOGIEFHTRLQPGYFGKDSFNVWGNQVYETRPSIGSSKT 376	
Qy 224 RDWTRYNQFRRSLTITLTDIVALFPNDSRRPRTYSQLTRBYITNPV---LENFDG 278	Db 224 RDWTRYNQFRRSLTITLTDIVALFPNDSRRPRTYSQLTRBYITNPV---LENFDG 278	Db 279 SFRGAGGERSRSPHMIDTINSITYDAHRYY-----YWSGHOIMASVGFSGPSE 332	
Qy 321 TFLS---JENSTRKPHLFDVLOGIEFHTRLQPGYFGKDSFNVWGNQVYETRPSIGSSKT 376	Qy 377 ITSPFYGDK---STEPVQKLISFD-GQKVYRTIANTDVAAMPNGKTVLGTYKVDQSQYDQKN 434	Db 333 FTFLPYCTGMGNAAPOORIVAUQGQVYRTLSST---FYRRFNFIGINNOQQLSVLDSTEF 388	
Db 229 SFRGAGGERSRSPHMIDTINSITYDAHRYY-----YWSGHOIMASVGFSGPSE 332	Db 333 FTFLPYCTGMGNAAPOORIVAUQGQVYRTLSST---FYRRFNFIGINNOQQLSVLDSTEF 388	Qy 435 ETSTQT-----YDSKRNNGHYSQADSIDQLPPTEDBPLEKAYSHOUNYABCFMLQDRR 488	
Qy 377 ITSPFYGDK---STEPVQKLISFDGKVYRTIAN---TDAAMPNGKTVLGTYKVDQSQYD 430	Db 339 AVGTSSNULPSAVY---RKSCTV---DSLDEFPPQNNVPQPROFSRSHVYSMF---RS 438	Db 399 AVGTSSNULPSAVY---RKSCTV---DSLDEFPPQNNVPQPROFSRSHVYSMF---RS 438	
Db 333 FAPFLFGAGNAAPPVLSUTGUGIPTRLISSPLYRRLIGSPBPNQELFVLDGTERFAS 392	Qy 489 GT-----IPFETWTWHSYDFFENTIAKTTQLPVVKAYALSQGASITIEPGFTGCNL 540	Qy 489 GT-----IPFETWTWHSYDFFENTIAKTTQLPVVKAYALSQGASITIEPGFTGCNL 540	
Qy 431 DQKNETSTQTYDQRNNGHVAQDSDIDOLPPTEDDEPKAYSHOUNYAECPFLMODRGT 490	Db 439 GSSSVSILRAPMFSWTHRSAEENNITASDSTQIPAVKGPNFLNG-SVISEGFTCGDL 497	Db 439 GSSSVSILRAPMFSWTHRSAEENNITASDSTQIPAVKGPNFLNG-SVISEGFTCGDL 497	
Db 393 LTNLPLST---IYQRQTV---DSLDTIPPQONSUPPRAGSHRSHVHT---MLSQAGA 443	Qy 541 LEIKESSNSIAK---PKTTLNSAALLORYVRIRYASTTINURFLQNSNDLVLVYINKT 597	Qy 541 LEIKESSNSIAK---PKTTLNSAALLORYVRIRYASTTINURFLQNSNDLVLVYINKT 597	
Qy 491 I----PFETWTWHSYDFFENTIDAEEKTQLPVVKAYALSQGASITIEPGFTGCNLFLIKE 545	Db 444 VYTLLRPTFSWQIRSAENNIIPSSQITQPLTKSTNLSGTSVVKSPGFTCGDL-RRT 502	Db 498 VRLNSCENNINQNRGYLEVPIHPSTSTRYRVRYASVTPITHLNWGNSSIFNSTVTPAT 557	
Db 444 VYTLLRPTFSWQIRSAENNIIPSSQITQPLTKSTNLSGTSVVKSPGFTCGDL-RRT 502	Qy 546 SENSIIAKPKTTLNSAALLORYVRIRYASTTINURFLVQO-----NSNNDFLVYINKTMN 599	Qy 598 MNKDDDLITYQFDLATNSNGFGSDKNEELIGAEPSNSNEK1YIDKIEFIPV 650	
Qy 546 SENSIIAKPKTTLNSAALLORYVRIRYASTTINURFLVQO-----NSNNDFLVYINKTMN 599	Db 503 SPQSIQSTVRVNT-TAPI.SQYRVRIRYASTTINURFLVQO-----FSRATS 555	Db 558 ATSLDNL-QSSDFGYFESANFTSSLGN-IVGRVNFSGTAVQIDREFEFIV 607	
Db 503 SPQSIQSTVRVNT-TAPI.SQYRVRIRYASTTINURFLVQO-----FSRATS 555	Qy 600 KDDDLITYQFDLATNSNGFGSDKNEELIGAEPSNSNEK1YIDKIEFIPV 652	RESULT 36	
Qy 556 SGSNLQSGSSFRTVGFTPEFNFSNGSSVTLSAHVFNSNEVIDREFVPAEV 608	Db 556 SGSNLQSGSSFRTVGFTPEFNFSNGSSVTLSAHVFNSNEVIDREFVPAEV 608	S32649 parasporal crystal protein cry1Fa3 - Bacillus thuringiensis	
RESULT 35		C;Species: Bacillus thuringiensis	
S11445 parasporal crystal protein cry1A.c - Bacillus thuringiensis _B		C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004	
C;Species: Bacillus thuringiensis _B		C;Accession: S32649	
A;Variety: strain Bts89A		R;Lambert, B.	
Ci;Accession: S11445		Submitted to the EMBL Data Library, April 1993	
Ci;Date: 21-Nov-1993 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004		A;Reference number: S32645	
C;Cross-references: UNIPROT:Q45737; EMBL:X54159; PID:g40274; Pred. No. 33.3%; Mismatches 112; Indels 64; Gaps 16		A;Status: preliminary	
A;Experimental source: strain Bts89A		A;Molecule type: DNA	
A;Note: In the authors' translation 75-Ala is shown after residue 83 and, consequently, C;Superfamily: Parasporal crystal protein		A;Residues: 1-117 <DAR>	
C;Keywords: delta-endotoxin		A;Cross-references: UNIPROT:Q45749; EMBL:Z222512; PID:g295865; Pred. No. 5.9e-46%; Mismatches 220; Indels 64; Gaps 16	
A;Molecule type: DNA		A;Cross-references: UNIPROT:Q45749; EMBL:Z222512; PID:g295865; Pred. No. 5.9e-46%; Mismatches 220; Indels 64; Gaps 16	
A;Residues: 1-618 <DAR>		Query Match 25.3%; Score 861.5; DB 2; Length 618;	
A;Cross-references: UNIPROT:Q45737; EMBL:X54159; PID:g40274; Pred. No. 2e-47; Mismatches 111; Indels 81; Gaps 24;		Best Local Similarity 33.5%; Pred. No. 2e-47; Mismatches 111; Indels 81; Gaps 24;	
A;Experimental source: strain Bts89A		Query Match 25.3%; Score 861.5; DB 2; Length 618;	
A;Note: In the authors' translation 75-Ala is shown after residue 83 and, consequently, C;Keywords: Parasporal crystal protein		Best Local Similarity 33.3%; Pred. No. 5.9e-46%; Mismatches 112; Indels 64; Gaps 16	
C;Cross-references: UNIPROT:Q45749; EMBL:Z222512; PID:g295865; Pred. No. 5.9e-46%; Mismatches 220; Indels 64; Gaps 16		Query Match 25.3%; Score 861.5; DB 2; Length 618;	
A;Cross-references: UNIPROT:Q45749; EMBL:Z222512; PID:g295865; Pred. No. 5.9e-46%; Mismatches 220; Indels 64; Gaps 16		Best Local Similarity 33.3%; Pred. No. 5.9e-46%; Mismatches 112; Indels 64; Gaps 16	
A;Cross-references: UNIPROT:Q45749; EMBL:Z222512; PID:g295865; Pred. No. 5.9e-46%; Mismatches 220; Indels 64; Gaps 16		Query Match 25.3%; Score 861.5; DB 2; Length 618;	
A;Cross-references: UNIPROT:Q45749; EMBL:Z222512; PID:g295865; Pred. No. 5.9e-46%; Mismatches 220; Indels 64; Gaps 16		Best Local Similarity 33.3%; Pred. No. 5.9e-46%; Mismatches 112; Indels 64; Gaps 16	
A;Cross-references: UNIPROT:Q45749; EMBL:Z222512; PID:g295865; Pred. No. 5.9e-46%; Mismatches 220; Indels 64; Gaps 16		Query Match 25.3%; Score 861.5; DB 2; Length 618;	
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A;Cross-references: UNIPROT:Q45749; EMBL:Z222512; PID:g295865; Pred. No. 5.9e-46%; Mismatches 220; Indels 64; Gaps 16		Best Local Similarity 33.3%; Pred. No. 5.9e-46%; Mismatches 112; Indels 64; Gaps 16	
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Db	322 HLVNSFRGTTTINJRSPLRPTVPTISAPSVPVIFERULSYFGLNNNNPVA--- 378	Db	384 DGERICLNLKLGQQPYTEK----APVVDSPPIRIPONNNPPRGTSFHRCLAYVSNF 438
Qy	414 NGKTYLGVTKVDFSDQDKNETSTOTYSKRNNGHVSAQDSDQLPPTTDBPLEKAYS 473	Qy	483 LMQDRGRTIPFF----TWTHRSDVFENTIDAEEKITOLPVVKAVALSSGA-SIEGPG 534
Db	379 -----GIEVEP-----QNTISRSIY---RSKSPI---DSESELPPDVSVPAIGS 420	Db	439 YSGFSNNSSVSVIRAPNDSSWTCASEFGDVIPSQITQPLTK--LOGWLWNSVKGGLG 495
Qy	474 HOLNYAECLMQR----RGTPPFWTWRSVDFENTIDAEEKITOLPVVKAVALSSGAS 529	Qy	535 FTGCGNLLEKEKSSNIAFKVTLNSSAALLQRYVRVIRASTTMVLRLFVQ----NSNND 588
Db	421 HRLCHA-TFLERISPRIGTV--FSWTRSSASPINEVSPSRITQIPWRAHTLASGAV 477	Db	496 FTGCGDI--LEELTGQISTLRVNI-TAPLSQVRVVRVIRASTTMVLQFHTSIDGRP1QGN- 551
Qy	530 IEGRGFTGCNLNLKEKSSNIAFKVTLNSSAALLQRYVRVIRASTTMVLRLFVQNSNNDP 589	Qy	589 FLVIYIKNTMKNDLTYQTFDLATTSNMGFGCDKNELIGAESFVNENKIVYKIDKIEP 648
Db	478 IKGPFETGCGDL-TRNSMDGLGALRVTFTGRLQSYTFRASVANRSGTRYSOPPS 535	Db	552 ----FSATMSSGSNLQSGSFRTVGFPTPFNFSNGSSVFTLSAHVFNSGNEVYDRIEFV 606
Qy	590 LVVYINKTMANKDDDLTYQTFDLATTNSSNGPFGDKNELLIGAESFVNENKIVYKIDKIEP 649	Qy	649 PVOL 652
Db	536 YGLSPKTMNDAGEALTSRSFAHTTLFTPP-TFSRAQEFPFLYQS-----GUYIDRIBETP 590	Db	607 PAEV 610
Qy	650 V 650		
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R;Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Walfield, A.M.J. Bacteriol. 166, 801-811, 1986			
J;Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticida			
A;Reference number: A94672; MUID:86223796; PMID:3011746			
A;Accession: A29838			
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C;Accession: A29838		Matches 212; Conservative 116; Mismatches 233; Indels 98; Gaps 26;	
R;Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Walfield, A.M.J. Bacteriol. 166, 801-811, 1986			
J;Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticida			
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C;Superfamily: delta-endotoxin			
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A29838	parasporal crystal protein - Bacillus thuringiensis subsp. kurstaki	Query Match 23.8%; Score 809; DB 2; Length 1156;	
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C;Accession: A29838		Matches 212; Conservative 116; Mismatches 233; Indels 98; Gaps 26;	
R;Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Walfield, A.M.J. Bacteriol. 166, 801-811, 1986			
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J;Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticida			
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C;Superfamily: delta-endotoxin			
RESULT 39			
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C;Species: Bacillus thuringiensis subsp. kurstaki		Best Local Similarity 31.9%; Pred. No. 1.2e-43; Length 1156;	
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J;Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticida			
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A29838	parasporal crystal protein - Bacillus thuringiensis subsp. kurstaki	Query Match 23.8%; Score 809; DB 2; Length 1156;	
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R;Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Walfield, A.M.J. Bacteriol. 166, 801-811, 1986			
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R;Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Walfield, A.M.J. Bacteriol.			

FEBS Lett. 293, 25-28, 1991
A;Title: Nucleotide sequence of a novel delta-endotoxin gene cry9 of *Bacillus thuringier*
A;Reference number: S19306; MUID:9207058; PMID:1660003
A;Accession: S19306
A;Cross-references: UNIPROT:Q9031; EMBL:X58120; PIDN:CAA41122.1; PID:g40271
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A;Accession: S23588
A;Molecule type: protein
A;Residues: 24-34 <SM0>
A;Experimental source: subsp. *Galleriae*
R;Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.
J. Gen. Microbiol. 138, 55-62, 1992
A;Title: Identification of an insecticidal crystal protein from *Bacillus thuringiensis* D5
A;Reference number: A44847; MUID:92211329; PMID:1565566
A;Accession: A44847
A;Status: preliminary
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A;Residues: 1-1151 <GLB>
A;Cross-references: EMBL:X58534; PIDN:CAA41425.1; PID:g48880
C;Accession: B42459
R;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene from *Bacillus thuringiensis* - strain aizawai (frag
A;Reference number: A42459; MUID:91286178; PMID:2061280
A;Accession: B42459
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Matches 197; Conservative 129; Mismatches 292; Indels 64; Gaps 21;
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2 NQNKHGIGIAGSNCGACSDDVAKPLANNP-----TSSALNLNSCONSSSLNWINITG 53
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Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 1 MNPNPRNSEHTDI -----KVTNSELQTHNHQYPLADNPNSTLEBLNYKEFLRMTEDSS 53
Db 1 MKLNPPDKHQSPSNKVKDTS-----LKNETDIEQNLINHEDCUKLSEYEN 50
Query Match Score 20.6%; Score 700; DB 2; Length 380;
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Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 54 TE-VLDNSTVKGTDKAVGTGISVGVQOLGVPGAGALTFSYQSFNLNTWPSADPWAEMA 112
Db 51 VEPEPVASATIQ---TGSIAKGKLGTIVGPFAQVSLYSLSFILGEMLPKGKNOWEIM 106
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Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
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Db 172 IEEYAKSKAELQGQIQQNFEDYVNALSWKKTPLSLRSKRSQDIRELFS 172
Db 173 QAESHFRNMRSPFAVSKEFVLPLPTYAQANTHILLKDAQVFGEEGYSSVEDAEEFYHR 232
Db 174 AELMFVQLQKSPFAVSKEFVLPLPTYAQANTHILLKDAQVFGEEGYSSVEDAEEFYHR 232
Db 175 QKLRLTQOYTDHCVNWNVNGLNGLSTYDAWKENREREMTLTVLDLIVLFPYDYL 292
Db 176 OVERAGDYSHCCKWYKSTGLNLRGTAWSWRYNQFKDMVLLDVALFPYDTLYV 283
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Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 177 QKLRLTQOYTDHCVNWNVNGLNGLSTYDAWKENREREMTLTVLDLIVLFPYDYL 292
Db 178 DAVGTGTSIVYGQILGVGVGPFGAGALTFSYQSFNLNTWPSADPWAEMA 112
Db 179 DAKEAVSVICRTIVSLLTAPSITLGLISIYDILGKVGGSSGQSISDLSCIDLISIDIR 113
Db 180 VSQVSLNDGIAFDNSVLLYRNLYEALDWNKNP---NSASABELRTFRIADEDFRI 169
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 181 LVEFLILTYDVCVHNNTARGFNLNRQGTSATAWLFHRVREMTLMVLDLVASFSSLDT 289
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 182 LYSKGVYKTELTRDIFDPFLSNTLQEQYGPFTFLS -----TENSIRKPHLFDYLOGI 341
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 183 NYPIETDFQLSRVITYDPIGVHRSLSRGESWFSFVNANSDELNAIPNPRSWFLNNM 349
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 184 RLQPFYFGKUSENWYSGNTVETRPSIGSSKTITSPFGKDKSTPQVQLSFDGQK 399
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 185 LISTGSLTLPVSPSTIRARYWGS - RDRISPANSFITELISGHTATQOTIL --GRN 404
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 186 405 IFR ---VDSQACNLNDTTYCVNRAVF - YHDASBQSRSVYEGTRTGTIDNPVQVNIN 458
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 187 DQLPPEITDEPKAYSHQLNAYABC -----LMQBRGTTI PFTWTHRSYDFENTIDAE 510
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 188 459 TYLPGENSDIPTPEDTHLSTINTTGGLRQVASNRSSSLAKFKVTLNSALLQRVRVRI 570
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 189 511 KITOLPLVYKVALSSGASIEPGFPTGNNLFLKEFSSNSSLAKFKVTLNSALLQRVRVRI 570
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 190 512 RTQIPLKVDTRGTVGTVYNDPGFLOGALLQRTBHGSGLGVLRV-QPLHLRQQRIRV 576
Query Match Score 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.e-35;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Db 191 571 RYASTTNLRLFVQNSNNDFLVYIN - KTMNKDDDLTYQTPDLATNSNMGFSGDNLIELI 628
R;Smulevitch, S.V.; Shavellev, A.L.; Osterman, A.I.; Kadry

RESULT 42

S19306

parasporal crystal protein cry9Aa1 - *Bacillus thuringiensis*

parasporal crystal protein cry9Aa1; insecticidal crystal protein; parasporal crystal pro-

N;Alternative names: delta-endotoxin

C;Species: *Bacillus thuringiensis*

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004

C;Accession: S19306; S23588; A44847; S14602; S14337

R;Smulevitch, S.V.; Shavellev, A.L.; Osterman, A.I.; Kadry

Db	577 RYASINTNIRLUSV--NGSFCTISONLPSTMRLGEDLRYSGFAIRENTSIRTPASPQDQR 633	Db	587 PSSTRQENATDITYADEFGYTTEPRTVFNKTSEGDEDTLMLYGTPNHSYN--IYTOKI 644
Qy	629 IGAEEFVSNKEKIIDKIEFPV 650	Qy	646 EFIFPV 650
Db	634 LTIEPSFIQEVEVYDRIEFPV 655	Db	645 EFIFPI 649
RESULT 43			
B29838	parasporal crystal protein - <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> (fragment)	Db	587 PSSTRQENATDITYADEFGYTTEPRTVFNKTSEGDEDTLMLYGTPNHSYN--IYTOKI 644
C;Species: <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i>		C;Alternate names: delta-endotoxin Bt8; insecticidal protein ISRH3; mosquitoicidal 130K p	
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004		C;Species: <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i>	
C;Accession: B29838		C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004	
R;Thorne, L.; Garduno, P.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Walfield, A.M.		C;Accession: S00398; A37587; JT0315; A28541; J39869; I40584	
J.; Bacteriol. 166, 801-811, 1986		R;Chungitupornchai, W.; Hofte, H.; Seurinck, J.; Angsuthanaosombat, C.; Vaeck, M.	
A;Title: Structural similarity between <i>Lepidoptera</i> - and <i>Diptera</i> -specific insecticida		Eur. J. Biochem. 173, 9-16, 1988	
A;Reference number: A94672; MUID:86223796; PMID:3011746		A;Title: Common features of <i>Bacillus thuringiensis</i> toxins specific for Diptera and Lepid	
A;Accession: B29838		A;Reference number: S00398; MUID:88185334; PMID:2833395	
A;Molecule type: DNA		A;Accession: S00398	
A;Residues: 1-934 <THO>		A;Molecule type: DNA	
C;Superfamily: parasporal crystal protein		A;Residues: 1-1136 <CHTO>	
A;Cross-references: UNIPROT:P09632; GB:MI2662; NID:9143228		A;Cross-references: UNIPROT:P05519; EMBL:X07423; NID:940353; PID:940354	
Query Match 19.5% Score 665.5 DB 2; Length 934;		R;Yamamoto, T.; Watkinson, I.A.; Kim, L.; Sage, M.V.; Stratton, R.; Akande, N.; Li, Y.; N	
Best Local Similarity 20.0% Pred. No. 1.3e-34		Gene 66, 107-120, 1988	
Matches 210; Conservative 118; Mismatches 246; Indels 151; Gaps 34;		A;Title: Nucleotide sequence of the gene coding for a 130-kDa mosquitoicidal protein of <i>Bt</i>	
Qy	1 MNPFNNRSHBDTIKVTPNS-ELQTQHNHQPLADNPNSTLEELNKPEFLRDTED-----51	A;Accession: A37587	
Db	1 MNPFQNKNYEIEFNAPSNQFSKSNNYSRPLANKPNQPKNTKYNKDMLNCQDNQQGNM 60	A;Molecule type: DNA	
Qy	52 ---SSTEYLDNSTVKDAVGTGTGIVSVQGQQLGVWGVPPFAGALTTSFYQSFLNTIWPSDADPW 107	A;Residues: 1-50 'D', 52-64 'S', 66-192 'PHKCTRMVY', 202-204 'C', 207-374 'I'	
Db	61 AGNPFASSETI-----VGYSAGIIVVGTMILGAPVLAQVLAGITISPGTLPIFM-QGSDPA 113	YKEFLEBQRLQNYV', 573-593, 'N', 595-686, 'GLIS', 691-720, 'R', 722-822, 'LIVSVVRCA', 833-835, 'WD',	
Qy	108 KAFKAQVEY-----LIDKIEEYAKSKVALAELQGLNNFEDTYNALNSWKTPLSLRSK 161	A;Cross-references: GB:M20242; PID:9142737; PID:AA22337-1; PMID:2901387	
Db	114 NWQDQNLNGGRPQEBIDKNIINVLT-----IVTPRKNDKYQEFFDWEP-----RTIH 165	A;Accession: JT0315	
Qy	162 RSQDRIREFSQAE-----SHPRNMSMSPAVSKFEVFLPPTYQAQANTHLLKLQDQV 214	A;Molecule type: protein	
Db	166 ANAKAVHDIFTLEPLIIDDLMLKNN-----ASYRIFTLPAYAQATWHNLNLKHAAT 219	A;Residues: 1-13 <YA2>	
Qy	215 FGEW-----GYSSEDVAFYHRQLK-LTQQTIDHCYVNWYNGLNGLRGSTYDAWYKPN 267	A;Note: the majority of sequence differences are consistent with frameshift errors	
Db	220 YYNWLQNGINPSTENNSNYQCYLKRKIQETDYCQTYNAGLTMIRTNTNATWMMY 279	R;Tungpradubkul, S.; Settasatien, C.; Panayim, S.	
Qy	268 RFREEMTLYLTDIYLVLFPYDIRLYSKGKTBTELTRDIDPFLSPLNTLQEQYGPFTLSI 327	Nucleic Acids Res. 16, 1631-1634, 1988	
Db	280 TYRLBMTLTVLDLIAFPYDPEKYGKSELREYT-----NVNSDTPRTITEEN 333	A;Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal genes c	
Qy	328 SI-RKPHLFQYLQGIEFHTR----LQPFYFGKDFSENY-----WS--- 361	A;Reference number: I39869	
Db	334 GLTRNPLTFWINGGRFTRNSRBDLDP---YDIFSTGNOMAFTHTNDDRNLIWGAH 389	A;Accession: I39869	
Qy	362 GNYVETRPPIGSKTTTSFYGDKSTPEVQKLSFDGQKVYRTRANTDAWPNGKVYLG 421	A;Sequence: translated from GB/EMBL/DBJ	
Db	390 GNII-----SQTDSKVF--PYFRNK--PIDKVAEVIRREYSDI-----IV--- 425	A;Molecule type: DNA	
Qy	422 TKYDFSQYDQKNETSTQTYDS--KRANGHVSQAQDSIDQLPPTTDEPLERAYSHQLYNA 479	A;Residues: 1-142 <RG2>	
Db	426 EMIFFSNSSBEVFRYSSNSTIENNNYKRTDSYM-----IPIKPTWK---NNEEYHTSY 474	A;Cross-references: EMBL:X05692; NID:940350; PID:940354; Score 656.5; DB 1; Length 1136;	
Qy	480 EC----FLMQDRRGTTIPPTWTHRSVDFENTIDAEEKTQLPVKAYALSSGASIIFGP 534	Best Local Similarity 28.3%; Pred. No. 6..6e-34; Matches 188; Conservative 140; Mismatches 260;	
Db	475 KTDNYIFSVRERRVA-FSWHTTSVDFQNTIDLDNTQTHALKALKVSSDSKIVKGPG 532	Matches 188; Conservative 140; Mismatches 260;	
Qy	535 FTGNNLFLFKESSNSIAKPKVTNSAALLQYRVRVIRVASTNRLFVQNSNANDFLVYI 594	Score 65.5; DB 1; Length 1136;	
Db	533 HTGDLVVIKDSMDPRVRFLEKNS----RQYQVIRYTA-TNAPKTTVFLGTDITISVEL 586	C;Comment: This protein is toxic to many lepidopteran larvae.	
Qy	595 NKTMNKDD---DLTYQFFDLAT---TNSMGFSGDKNEL--LIGAESFSNEKUYDKI 645	C;Superfamily: parasporal crystal protein	
Db	5 YPLADNPNSTLELNKTYKEFLRMTEDSSTEVLDNSTV-KDAVCTGIGSVQIQLGVGVGPFA 85	C;Keywords: delta-endotoxin	

Qy	86 GALTSPYQSLNFTIWPSDADP----WKAFAAQVEVLIDKIEEYAKSKALAELOGLQNFF 141	Db	61 FEPFIDSGELSAYTIVGTVLTGFFTPGLALLGP-GTLIPVLFPAQDQSNTWSIFIT 119
Db	64 GTVLTVLSAVLPILWPTINTPPVERVINDFTNTGMLIDQTYTAYTAYRTDANKMTVVKDYL 123	Qy	113 QVEYLIDKKEEYAKSKALAELOGLQNFFDTYNALNSWKUPPLSRSRKSODPRIRLEPS 172
Qy	142 EDYVNAALNSWCKTPELRSRSRSQRDRFLFSQAESHRNMSPSA-VSKPEVFLPTYAO 200	Db	120 QTNNIIRGEIASTYVSNANKILRSRNPNTVSYHNLKTWNNP--NPONTQD-VRTOIQ 175
Db	124 DQYTTRKENTWRREP---NNQSYRTAVITQFNLTSALKRETAVYFSNLVGFELLPLPIAQ 180	Qy	173 QAESHERNSMPSFAVS-----KEFVLFPTYAOAANTHILLIKDAQVF----GE 217
Qy	201 AANTHILLIKDAQVFQGVGEWGYSSSEDAEFYHRQLKLTOQYTDHCYVNWYNGLNRGSITY 260	Db	176 LVHVFQNTIPELYNSCPNPSPDDYNNLILVLSYQAQNLHVTVLNOAVKFAYLKXNR 235
Db	181 VANFNLLIRIDGLINAQEWSSLARSAGDQLNTMVQYTKETIAHSITWNGLDVRNKS 240	Qy	218 EWGYSS--EDVAEYFHQLKLTOQYTDHCYVNWYNGLNRGSITYDA-----WVKFNR 268
Qy	261 DAWVKFNRFRRENTLTVDLIVLFPPTYDIRLY-----SKGVKTELTRIFTDPIESLN 313	Db	236 QFDYLEPLTAIDYPVLTKAIEDTYNCUTVYXKGGLNLK-TTPDSNLDGNNWNTNT 294
Qy	241 GOWITENDYKRENTQVLDLAFASDPRRYPADKIDNTKLSKTEFTRIYTALVESPS 300	Qy	269 FRRENTLTVDLIVLFPFDIYLXSKGVKTELTRIFTDPFLSNTLQEQYGPFTLSENS 328
Qy	314 TLQEYGPFTSIENSI-RKPHFLDYLOGIEPFHTR-----LQPGYFGKDSFNYWSGNVET 367	Db	295 YRTKMTATVLDLVLPNNDVGKPYQVSELTEBXYQVNLFNEESPVKYY-DFQYQEDS 352
Db	301 S-----KSIAALEAALTRDVHLFTWLKRDFWTNTIYQDLRFLSANKIGGSYTNSSAMQE 355	Qy	329 I-RKPHFLDYLOGIEFHTRLQ--PGYFGKDSFNYWSGNVETRPSIGSSKTRITSPFYGDK 385
Qy	368 RPSIGSSSKTITSPPYGDKSTEPMVQKLSFDDGOKYRTIANTDVAWNGKYLGVTKVDFS 427	Db	353 LTRRHLFLTWLSDSINFYEAKQTTPN-----NEFTSHYNMFMHTYLDNISQKSSVFGHNH 405
Db	356 SGYGGSS-----FGSNLTHIQIANS---NVYKT-STIDTSS-PSNR---VTKMDFY 399	Qy	386 STEPQKLSFSDGOKWYRTIANTDVAWPNPGKV-YLGTVTKVDF-----426
Qy	428 QYDD--QKNETSTQYDSCRNKN--GHVSAQDSIDQLPPTTDEPKAYSHOLNAYAECBP 482	Db	406 VTDKLUKSLGL-ATNVIYFLIN--VISLDNRYLNDNNNISRMDFFITNGTRLKELETAGS 462
Db	400 KIDGTLASYSNTNTPBGLRTTFFGFSTNEN-----TPNQPTVNDTHISYKD 451	Qy	427 -SQYDQDNNETSOTYDTSKRNGHVSQAQSDISDQLPPTTDEPKAYSHOLNAYAECFLM 484
Qy	483 LMODRRGTIPFTWTHRSVDFNTIDEKITOLPQVKAIALSSGASITIEGPGFTGCGNLLF 542	Db	463 GQITTDVNKNFQIGPLKERQENQNPFLPTYDN-----YHILSPKSLSLI 509
Db	452 VI-DYNSNRVSAWTHKIVDPNQIYDTAQPVAKVSNFNLTATAVKIGCQHTGCGDLVA 510	Qy	485 QDRRGT-IPPFPTWTHRSVDFPNTIDEKITOLPQVKAIALSSGASITIEGPGFTGCGNLLF 543
Qy	543 LKESNSNIAKFKVTLN8A---LQRYRVRIRYASTNLRL---FVQNSNNDFLVIVYINK 596	Db	510 PATYKTVQYPTPAWTHSVPDKNTIYTHLITQIOPAVKANSLGTTASKVYQGPFTGCGDLDF 569
Db	511 LTSGNTLSSGRMELQCTKTSIFNDPTRYGLIRYAAANSPIVLNVSYTLQGSRGTTISTES 570	Qy	544 KESSNSIAKFKVTLN8AALLQYRVRIRYAS---TTNLRLFVQNSNNDF-LVIVYINKMN 599
Qy	597 TMNKDD----DLTYCOTP---DLATTNNSMGFGSDKNELI---IGAESFVSNEKYYDKI 645	Db	570 KD-----HFKITCOSHNSFOOSYFIRYASNGSANTRAVINLSPGVAELGMALNPTFS 623
Db	571 TFRPRNNIPTDLKYEFRYKDPFDAIVPMRLS--SNQLTITAIQPLNMTSNNQVIIIDR 628	Qy	600 KDD-DLTYQTFDIALTNSMGFGSDKN----ELIIGAESFVSNEKYYDKIPIPV 650
Qy	646 EPIP 650	Db	624 GTDYNLTKYKDFOYLFESNEVKFADNQNTSLVFNRSVYNTTVLIDKIEFLPI 677
Db	629 EIIPI 633		
		RESULT 46	
		A26858	parasporal crystal protein cry4Aa1 - Bacillus thuringiensis subsp. israelensis
		N;Alternate names: parasporal crystal protein cryIVa	
		C;Species: Bacillus thuringiensis subsp. israelensis	
		C;Date: 19-Nov-1988 #sequence_change 19-Nov-1988 #text_change 09-Jul-2004	
		C;Accession: A26858; S48601	
		R;Ward, E.S.; Ellar, D.J.	
		R;Nishimoto, T.; Yoshihisa, H.; Ihara, K.; Sakai, H.; Komano, T.	
		A;Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding ε	
		A;Reference number: A26858; PMID:88015571; PMID:2821500	
		A;Accession: A26858	
		A;Molecule type: DNA	
		A;Residues: 1-1180 <WAR>	
		A;Cross-references: UNIPROT: P16480; GB:Y00423; NID:940351; PMID:CAA68485_1; PMID:940352	
		A;Note: the authors translated the codon GCA for residue 308 as Thr	
		R;Nishimoto, T.; Yoshihisa, H.; Ihara, K.; Sakai, H.; Komano, T.	
		FEBs Lett. 348 : 249-254, 1994	
		Agri. Biol. Chem. 52 : 873-878, 1988	
		C;Superfamily: parasporal crystal protein	
		C;Keywords: delta-endotoxin	
		A;Reference number: 139869	
		A;Accession: S48691; PMID:94307434; PMID:7913448	
		Query Match Score 18.7%; Length 1180;	
		Best Local Similarity 27.6%; Pred. No. 1..le-32;	
		Mismatches 197; Conservative 129; Indels 101; Gaps 28;	
Qy	1 MNP-NNRSHDHTIKVTPNS-ELQTNHNNQPLADNPNSTEELNYKEFURMTEDSSTEVL 58	Db	1 MNPNQKNEVETLNASQKKUNISNNYTRPIENSPKQLQSTNPKDMLNMCQONQQYGGD 60
Qy	59 NSTYKDA--VGTGTSVVGQILGVYV--VDFAGALTSFYCSFLINTIWPS--DADPWKAFA 112		

Query Match	Score	DB 2;	Length
Best Local Similarity	26.7%	Pred. No.	3-9e-23;
Matches	157;	Mismatches	234;
Qy	84	FAGAITSFY-QSFLNTIW-PSADPWNKAQVEVLIDRKIERYAKSKALAEGLQNLN 139	
Ddb	35	FNNILTQDPLIITLISLWEDPNENBIRFSMIEDGETITKNLNSQTKEGILLNSNSPGL 94	
Qy	140	NFEDYVNALNSW--KKTPSLRSKRSDQIRELFSQAESHFRNSMSPSPAVSKFEVLFPLT 197	
Ddb	95	KFKYNNAFARSWIDVNYPNTSI-----DDVVYRPKDVNSICENNINEFKVKNYETVLP 148	
Qy	198	YAQDANTHILLLRDKAQVGEIEW-----GYSSEDVAEFTHRQLLTQQTDHCVNWWNG 251	
Ddb	149	YMQTANLHULLRDGMIGYGDAWNLYRELFQSFSDQQ-----SFTVNVHLDKTKPVINDCLNYNTG 206	
Qy	252	LNGLRGSTYDAWKYFNRFREMTLTVLDLIVLFPEFIRLYSKGVKE-LTRDIFTDPF 310	
Ddb	207	LSNIKLDPNNSWIDITYCRFMTYILDMSICPIYDTKYDQPIMQMOTLTKVYSDPV- 265	
Qy	311	SINTLQEYGPFTLSEINSRSTKPHFLDYLOGIEFHTRLQPSYFGKDSFNYWSG--NNVET 367	
Ddb	266	--NPIDENIPSEYEMMNISPFLSFISFYTNSKSNKFNLGHNRHGTDUNLYNGL 323	
Qy	368	RPSIGSKTITSPTPYGD-KSTEYQKLSFDQKVRRT--IANTDVAWPNGKVTLGVTKV 424	
Ddb	324	RET----HYGNIGNSNEYEVESMAFDIKAYSSNNFNNTQ---INNPNPTSYSKSIKF 369	
Qy	425	DFSQYDQ--KNESTQTYDSKRN-NGHVAQSDSIDOLQPETTDEPLEKASHOLNAYAEC 481	
Ddb	370	LITKNDNDEVITYGEPDSNIDFTRNIGYISLNNN-----BSYTHSL--SDM 413	
Qy	482	FLMDQRGTIPF----FTWTHRSDVFNTIDAEEKITOLPVVYKAVALS---SGASII 530	
Ddb	414	ILANNDKIQINIDTPHASYSYTWYKGIEDTNYTSKDLANQIPLYKEVKLKSRHYSEISVI 473	
Qy	531	EGPQPTGNNLFLIK--ESSNSI---AKFVKTL---NSAALLORYVRIRYASTTNLRL 580	
Ddb	474	KGPFCFTGPDLISKVHKPANQIPAQYMKNKITIPIKTKPAGSQDFVRLCYASNHDIGL 533	
Qy	581	EVQNSNDPLVYINKTMNKD-----DDLTQTFD-LATLNSNM 618	
Ddb	534	IRLIAGSKVITNIQQFNTENNPSPLYDDPKYFNFNETLSTITSSGI 581	
RESULT 48			
TI:18211 delta endotoxin - <i>Bacillus thuringiensis</i> (fragment)			
C:Species: <i>Bacillus thuringiensis</i>			
C:Accession: T18211 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004			
R:Poncearada, L.; Narva, K.E. Submitted to the EMBL Data Library, January 1995			
A:Description: <i>Bacillus thuringiensis</i> PS8603 delta endotoxin.			
A:Reference number: T18211			
A:Accession: T18211			
A:Status: preliminary; translated from GB/EMBL/DDBJ			
A:Molecule type: DNA			
A:Residues: 1-1245 <FON>			
A:Cross references: UNIPROT:Q45712; EMBL:U19725; NID:9862636; PID:9862637; PID:N- C:Keywords: delta-endotoxin			
Query Match	Score	DB 2;	Length
Best Local Similarity	21.8%	Pred. No. 1e-09;	Length 1245;
Matches	154;	Mismatches	241;
Qy	70	ISVVGQIUGVGYPAGALTSPYQSFNLNTIWP-----SDADPKAFMAQEVILDK 120	
Ddb	77	ISLIGFI-----PGAAEAVPFINMFVDFWPKLFGANTEGKDQQLFNAIMDAVNMKVVDN 130	
Qy	121	KIEBYAKSKALAEGLQNLNFEDYVNLN-----SWKTKPLSLRS-KRSQ 164	
Ddb	131	KELSYNLSLNLKTYTEGQNLGLEQNAIQCOSTSPERVNFDQNCPTPNQPCQKDDL 190	

Qy	165 DRIELPQSQAEHFRNSMSPF-----AVSKFE----VLFPLTYAQAAANTHLILKDA 212	Db	50 VAPVPGTVSSFLUKKGSLLCKRILSELWGLIIFPPGSTMNLQDILR----- 95
Db	191 DRASRFDTANSPTQHPEFKNPWSDENSTOKRTSVLTLPLMVTATLHLLYEGY 250	Qy	112 AQVEVILDKKLEAYAKSKAALLOGIQNNFEDY---VNAIN-SWFKTPPLSLRSKRSQDR 166
Qy	213 QYFGEENCGYSSSEDAEFTHRQLKLTTQYTDDHCYN-----WYNGLNGLRGSTYDAW 264	Db	96 -ETEQFVINQRINTDTLARVNELIGQANTRFPNQVDNFNLPNTQNPVLISITS--SVNT 152
Db	251 IEFMTKWNFHNEQ---YLNLNUKVELQQLIHSYSETVRTSFLQFLPLNRSKSSTNA-- 304	Qy	167 IRELPSQAESHFRNSMSPFAVSKFEVFLPTYAQAAANTHLILKDAQVFGEWGYSEDV 226
Qy	265 KPNFRREMMLTFLDLIVLFPFDIYLRSKGVTTELTDIDPFLSNTLQBYGPTFLS 324	Db	153 MQO-----FLNRLPQFOQYQQLLPFAQANMHSFIRDILNADEWGIAATL 205
Db	305 -YNRVYRNMTVNCNDIAATWPFDTMHYHQGKLDLTRLSD---TAGPIEYFTG-- 357	Qy	227 AEFYHQLKLTOQYTHCUNVYNGLRLGSTYDWWKFNFRRMILTLFLDLYLFPF 286
Qy	325 IENSIRKPHFLDYLOGIEBFHTRLQPGYFGKDSFNYNSGMQVNVETRPS---IGSSKTKITSPF 381	Db	206 RTYRDYLRLNTYTRDYSNCINTYQTAERGLNTRLHD---MLEFRTMFLNVEYXWSL 261
Db	358 -----DKTSGPB-HSNTP-----NNLDT-PSTPYQHSFVSDSI V 392	Qy	287 YDIR-----LXSGKVBLTRDI-----FTPPIFSANT---LOEYGPFTFLIENS 328
Qy	382 YGDKSTPEVQKLSFDGQKVRYTANTDVAWPNGKVYLGVTKVDFSOYDQKNE---TS 437	Db	262 FKYQSLMVSSGANLYASGSQGQQTQSFATAQNWPFLYSLFQVNSNLYLISGSTRLSI-- 318
Db	393 YSRKELOODIATYS-----TNNSNNCHPYG---LRLSTYDGSRYDQCDNBQDPFTTS 441	Qy	329 IRKPHFLDYLOGIEFPHTRLQPGYFGKDSFNTYQTAERGLNTRLHD---SSGKSYGDKSTE 388
Qy	438 TQTYDSKR-----NNGHV-SAQSDIDL-----PPEI 463	Db	319 -----TPPNICL-----PGSTTHSLMSARVN-----GGVSSGLIGATNLN 357
Db	442 NNNYCHNSYATTPLTLYNARHLYAKGSLQNEVSLSVYSTVNGSGSCTCDAWINYLRPPF 501	Qy	389 PVQKLSFDGQKVRYTANTDVAWPNGKVYLGVTKVDFSOYDQKNE---TQYDSKRNNG 448
Qy	464 T-----DEPLEKAYSHQQLNTABCFLMQDRRTIPFTWTHRSVDFENTI 507	Db	358 H---NFNCSTVLPLPPLSTPPFVSLWDS---GTDREGVATSTNWQTB-SFQFTLSSLR-CG 407
Db	502 SKNECSRDPDKQINVLYLPTETVNGTGNGNLGVISAYPME---LVP-----ENV 547	Qy	449 HVSAQSIDQLPP---ETTDDEPL---EKAYSHQHLYAECPLMDQDRGT---IPPTWT 497
Qy	508 -DAEKITOLPV---VKAYALSSGASILEGPQF-----GGNLLFLKESNSNIAKFVTL 557	Db	408 AFSARGNSNTYFPDFYFFRNISGVPLVIRNEDELTRPLHYQNRINIESSGTPGGRARLVSV 467
Db	548 GDVNADPKLPLTQLGPFPEKYGSEYNRQGISLVRNINGNNA---VRLNSQSQVGQITN 605	Qy	498 HRSVDFENTIDA-----ERITOLPVVKRAYAL---SSGASIIIEGPFTGGNLL 541
Qy	558 NSAALLQRYRVRYASTNTRLPLVQNSNNDLFLVYINKTANKKODDLTYQFDLATTNS 617	Db	468 HNRK---NNIYAENGTMHHLAEPDYGFTISPIHATQVNQNQTRTFISEKFGNQODSLR 524
Db	606 QTK---QKYEICRYAS-----KGDSENPPRNSF-STESSV 649	Qy	542 FLKESSNSIAKFKVTLNSAALLQRYRVRYASTNTRLFLVQNSNNDLFLVYINKMNNKD 601
Qy	618 MGFSGDKNELI-----IGAESF---VSNE---KLYIDKIEFIP 649	Db	525 F---EQSNTARYTLRGNG---NSTNLYLRVSIGNTIRVTINGRVYTVSNVNTTNND 578
Db	650 VGVQGENGKYILKSLTIVEPAGSFYWHITNGQSSDSDLFLDRIEFVP 695	Qy	602 -----DDLTYQFDL ATTNSMGFSGDKNELIIGAESFVSNEKIY 641
<hr/>			
RESULT 49		Db	579 GVNDNGARFS DINIGNIVASDNTNTVLDINTVNTLNQCTPFD----- 618
C32053	parasporal crystal protein B1 - Bacillus thuringiensis subsp. kurstaki	Qy	642 IDKIBTPVQL 652
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C;Species: Bacillus thuringiensis subsp. kurstaki			
C;Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 09-Jul-2004			
A;Accession: C32053 ; A29913			
R;Widner, W.R.; Whitley, H.R.			
J. Bacteriol. 171, 965-974, 1989			
A;Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp. kurstaki		D32053	parasporal crystal protein B2 - Bacillus thuringiensis subsp. kurstaki
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A;Status: preliminary		R;Widner, W.R.; Whitley, H.R.	A;Status: preliminary
A;Molecule type: DNA		J. Bacteriol. 171, 965-974, 1989	A;Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp. kurstaki
A;Residues: 1-633 <WID>		R;Dankocsk, C.; Donov, W.P.; Jany, C.S.	A;Residue: 1-633 <WID>
A;Cross-references: UNIPROT:P21253		Mol. Microbiol. 4, 2087-2094, 1990	A;Cross-references: UNIPROT:P21254
R;Donovan, W.P.; Dankocsk, C.C.; Gilbert, M.P.; Gavron-Burke, M.C.; Groat, R.G.; Carlto		A;Molecule type: DNA	R;Dankocsk, C.; Donov, W.P.; Jany, C.S.
J. Biol. Chem. 263, 561-567, 1988		A;Title: Activation of a cryptic crystal protein gene of Bacillus thuringiensis subsp.	Mol. Microbiol. 4, 2087-2094, 1990
A;Title: Amino acid sequence and entomocidal activity of the P2 crystal protein. An inse		A;Residues: 1-633 <WID>	A;Title: Activation of a cryptic crystal protein gene of Bacillus thuringiensis subsp.
A;Reference number: A29913 ; MUID:88087146 ; PMID:3121615		A;Accession: S12396	A;Accession: S12396
A;Accession: A29913		A;Status: preliminary	A;Status: preliminary
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C;Genetics:			
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Best Local Similarity 21.8%; Pred. No. 5.6e-08;			
Matches 146; Conservative 96; Mismatches 258; Indels 171; Gaps 29;			
Qy	62 VRDAVGTG1SV----VQI1G-----VGVGPAGALTTSYQSFINTIWPSDADPWKA 111		

Query Match 7.2%; Score 245; DB 2; Length 633;
 Best Local Similarity 19.5%; Pred. No. 6.1e-08;
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Qy 83 PPGALTSE-----YQSFINTIWPS-DADPKAFMAQVEVILDKKIEEAKS 128
 Db 52 PIVETVASPLKKVGSIVKRILSELRLNIFPSGSTNLMDLIRETEKFNLQRINTDIA 111
 Qy 129 KALABLQQGJQNFPDDYVNLNSW----KKTPLSLRSRSQDTRLEFSQAESHFRNSMP 183
 Db 112 RVNAELTGQANVEEFNRQVDNFNLPNMRAPLTSI-SVNTMQL-----FLNLP 162
 Qy 184 SFAVSKFEYLFLPITYAQANTHLLKLKDPAQVFGEEMGYSEDVAEYHRQLKLTOQYTDH 243
 Db 163 QFQHQGYQULLPLPAQANLHLISFIRDILNADEWGSAAUTRITYRDLYQNTDVSNY 222
 Qy 244 CVMHYNVGNGLRLGSTDYDWVKENFREREMTLYLDLVLFPEYDIR-----LYSK 294
 Db 223 CINTYQSASFGLNLTRLHD---MLEFRYTMFLAYFEVSYISWLKYQSLVSSGANLYAS 278
 Qy 295 GVKFBLTRDI-----FTDPIFSINT-----LQEYGPFLSIENSIRKPHIF-- 335
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 Qy 336 --DYLQGIBFHTRLQPGYTKDSDFY----- 359
 Db 339 RVN5GGI-----SSGDGASPLQNPFCSTFLPPLTPFVRSWLDGSREGVATVN 392
 Qy 360 WSGNYVETPSI-----GSSKTITSSPYGDKSTEVPQKLSFDGQKVY-YRTIANTDV 409
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 Qy 410 AAWPNG----KYLGVTVDFSOYDDONNETSTQYDOSKRNGHVSQADS--IDQLPB 462
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 Qy 581 FVQN-----SNNDFLVYTINKTMKDDDLTYQTFDLATNN 615
 Db 574 TTNDGVDNDNGARFS DINIGNVASSNSDVLIDINVLNISGTOFDLMIMLVPTN 628

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